

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 08:59:36 ; Search time 4805 Seconds
(without alignments)
11104.115 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

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LOCUS AB3293 1231 bp DNA linear PAT 21-JAN-2000

DEFINITION Sequence 3 from Patent WO9850542.

ACCESSION AB3293

VERSION AB3293.1 GI:6732711

KEYWORDS

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 1231)

AUTHORS Giacobino, J. and Boss, O.

TITLE UNCOUPLING PROTEIN HOMOLOGUE: UCP 3

JOURNAL Patent: WO 9850542-A 3 12-NOV-1998; NOVARTIS ERINDUNGEN VERWALTUNG (AT); GIACOBINO JEAN PAUL (CH)

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| QY | 61 | CCACCGCTGCACCTGAAGCCCAAGGGCTGTGGAGCAAGCTCTCTCTTGGACCTCTCTCGG | 120 |
| Db | 61 | CCACCGCTGCACCTGAAGCCCAAGGGCTGTGGAGCAAGCTCTCTCTTGGACCTCTCTCGG | 120 |
| QY | 121 | CCCTAAGAGGACTGTGGGAGAGCTTCCAGAGACTGATGGTGGACTGAAGCTTCAAGCGTG | 180 |
| Db | 121 | CCCTAAGAGGACTGTGGGAGAGCTTCCAGAGACTGATGGTGGACTGAAGCTTCAAGCGTG | 180 |
| QY | 181 | CCTCCCAACATAGCTGTGAAGTTCTCTGGGGGACAGGACAGAGCGCTGTTTGTGAAGCTTC | 240 |
| Db | 181 | CCTCCCAACATAGCTGTGAAGTTCTCTGGGGGACAGGACAGAGCGCTGTTTGTGAAGCTTC | 240 |
| QY | 241 | GTTACCTTTTCACTGGAGACAGAGCAAGGTCCGCTGTGACAGATCCAGGGGGAGAACCAAGCG | 300 |
| Db | 241 | GTTACCTTTTCACTGGAGACAGAGCAAGGTCCGCTGTGACAGATCCAGGGGGAGAACCAAGCG | 300 |
| QY | 301 | GTCCAGAGCGGCCGGCTGTGCAATACCGTGGCGTGTGGGCAACATCCTGAACATAGTG | 360 |
| Db | 301 | GTCCAGAGCGGCCGGCTGTGCAATACCGTGGCGTGTGGGCAACATCCTGAACATAGTG | 360 |
| QY | 361 | CGGACTGAGGGGTCCTGGAGGCCCTTACATATGGGCTGTGGGCGGCGCTTGACGCGCAGATG | 420 |
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| QY | 721 | GCTATGTCTCACTGTGTCTGAGGTGTGACCTTACGACATCCTCAAGAGAAAGCTGTGGAC | 780 |
| Db | 721 | GCTATGTCTCACTGTGTCTGAGGTGTGACCTTACGACATCCTCAAGAGAAAGCTGTGGAC | 780 |
| QY | 781 | TAACAACCTGCTCACTGAACAATCCCTCGCTCACTTTGTCTCTGCTCTTGGAGCGCGCTTC | 840 |
| Db | 781 | TAACAACCTGCTCACTGAACAATCCCTCGCTCACTTTGTCTCTGCTCTTGGAGCGCGCTTC | 840 |
| QY | 841 | TGTGCAACAGTGTGTGCTTCCCGGTGGAGGTGTGAAAGACCGGGTATAGACTCACT | 900 |
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| Db | 961 | ACAGCCTTCTACAAAGGATTTACACCCCTCTTTTGGCTTTGGGATCTCTGGAACGTGTG | 1020 |
| Qy | 1021 | ATGTTGCTAACCTATAGACAGCGCTGAACCGGGCCCTGATGAAAGTCCAGATGTTACGGGAA | 1080 |
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| DEFINITION | Sequence 1 from patent |
| ACCESSION | AR381440 |
| VERSION | AR381440.1 |
| KEYWORDS | GI:40089474 |
| SOURCE | Unknown. |
| ORGANISM | Unknown. |

| REFERENCES | AUTHORS |
|---------------------|--|
| 1 (bases 1 to 1251) | Caplan, S. L., Boettcher, B. R., Slosberg, E. D., Connelly, S., Kaleko, M. |

TITLE Methods and compositions for treatment of diabetes and related conditions via gene therapy

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/mol type="genomic DNA"
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Query Match      100.0%;  Score 1231;  DB 6;  Length 1231;
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| Oy | 61 | CCACCGCTGCACCTGAAGCCCAAGGGCTGTGGAGCAGACCTCTCTCCTTGGACCTCCCTCTGG | 120 |
| Dp | 61 | CCACCGCTGCACCTGAAGCCCAAGGGCTGTGGAGCAGACCTCTCTCCTTGGACCTCCCTCTGG | 120 |
| Oy | 121 | CCCTAAAGGAGCTGGGSCAGAGCCTTCCAGAGACTATGATGTGAGCTAAAGCCTTCAGACGTG | 180 |
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 ACCESSION AR39364
 VERSION AR39364.1 GI:4011198
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 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
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AUTHORS Jacobino, J.-B., Muzzin, P. and Boss, O.
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HSU84763
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 VERSION U84763.1 GI:2183020
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1231)
 Bosse, O., Samec, S., Paoloni-Giacobino, A., Rossier, C., Dullio, A.,
 Seydoux, J., Muzzin, P. and Giacobino, J. P.
 Uncoupling protein-3: a new member of the mitochondrial carrier
 family with tissue-specific expression
 FEBS Lett. 408 (1), 39-42 (1997)
 JOURNAL FEBS Lett. 408 (1), 39-42 (1997)
 MEDLINE 97324095
 PUBMED 9180264
 REFERENCE 2 (bases 1 to 1231)
 Bosse, O., Samec, S., Muzzin, P., Rossier, C. and Giacobino, J. P.
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 Submitted (11-JAN-1997) Medical Biochemistry, Faculty of Medicine,
 University of Geneva, 1 Michel Servet, Geneva 4, GE 1211,
 Switzerland
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 DEFINITION Sequence 11 from Patent WO9852958.
 ACCESSION AX031190
 VERSION AX031190.1 GI:10278536
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 Chien, F. and Liu, Q.

TITLE Human uncoupling protein 3
 JOURNAL Patent: WO 9852958-A 11-26-NOV-1998;
 CHEN FANG (US) ; LIU QINGYUN (US) ; MERCK & CO INC (US)

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Query Match 97.7%; Score 1202.2; DB 6; Length 2340;
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 ACCESSION BD106811
 VERSION BD106811.1 GI:23201629
 KEYWORDS JP 2002502240-A/11.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Liu,Q. and Chen,F.
 TITLE Human uncoupling protein 3
 JOURNAL Patent: JP 2002502240-A 11-22-JAN-2002;
 MERCK & CO INC
 COMMENT PN JP 2002502240-A/11
 PD 22-JAN-2002
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 FH Key Location/Qualifiers.

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ORIGIN

Query Match 97.7%; Score 1202.2; DB 6; Length 2340;
 Query Similarity 99.6%; Pred. No. 8.2e-250;
 Matches 1226; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

1 TCCTGGATGAGCCCTAGAGAGCCCTGTGCTGCCCCCTGCGGAGAGAGCTCAGAGC 60
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| QY | 61 | CCACCGGTGACCTGAGAGCCCAAGGCGTGTGGAGAGAGCTCTCTCTCTTGAACCTCTCTCGG | 120 |
| Db | 106 | CCACCGCTGTGACTGAGAGCCCAAGGCGTGTGGAGAGAGCTCTCTCTCTTGAACCTCTCTCGG | 165 |
| QY | 121 | CCCTAAAGGGGACTGGGAGAGCCCTTGCAGAGACTATAGTGTGGACTGAAGCCTTCAGACGTG | 180 |
| Db | 166 | CCCTAAAGGGGACTGGGAGAGCCCTTGCAGAGACTATAGTGTGGACTGAAGCCTTCAGACGTG | 225 |
| QY | 181 | CCCTCCACCACTGAGCTGTGAGAGTTCTGTGGGGCAGGACAAGAGACCTGTGTTGCTGACTTC | 240 |
| Db | 226 | CCCTCCACCACTGAGCTGTGAGAGTTCTGTGGGGCAGGACAAGAGACCTGTGTTGCTGACTTC | 285 |
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| QY | 301 | GTCACAGACGAGCCGAGCTCGTGACAGTACCGTGGAGCGCTGAGGACACATCTGACCATGATG | 360 |
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| Db | 526 | GAGCGGGAACAATCCACAGCCTCATACCCGAGATTTTGGCCGACTGACACACAGAGCCATG | 585 |
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| Db | 766 | GCTATGCTCAACTGTGTGTGAGGTGTGACTTACGACATCCTCAAGAGAGAGCTGTGAC | 825 |
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ACCESSION AX175157
VERSION AX175157.1 GI:14598561
KEYWORDS
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ORGANISM Homo sapiens
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REFERENCE 1
AUTHORS Clapham, J.C.
TITLE New use
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JOURNAL SMITHKLINE BEECHAM PLC (GB)
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Best Local Similarity 99.9%; Pred. No. 1e-237; Indels 0; Gaps 0;
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DEFINITION AX361226
ACCESSION AX361226
VERSION AX361226.1 GI:18693870
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Clapham, J.C.
TITLE New use
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 AUTHORS Beelley,L.J., Paine,K. and Godden,R.J.
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 JOURNAL Patent: JP 2002300891-A 1 15-OCT-2002;
 SMITHKLINE BEECHAM PLC
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 ACCESSION ARI29842
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES Unclassified.
 1 (bases 1 to 1192)
 Beeley, L. James, Paine, K. and Godden, R. James.
 Polynucleotides and polypeptides belonging to the uncoupling
 proteins family

JOURNAL Patent: US 6187560-A 1 13-FEB-2001;
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Query Match 93.0%; Score 1145.4; DB 6; Length 1192;
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| QY | 1021 | ATGTTCTGTAACCTATGAGCAGCTGTAACAGGGCCCTGATGTAAGTCAGATGTTACGGGAA | 1080 | |
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| ACCESSION | AF001787 | | | |
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| SOURCE | Homo sapiens (human) | | | |
| ORGANISM | Homo sapiens | | | |
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| AUTHORS | Vidal-Puig,A., Solanas,G., Grujic,D., Flier,J.S. and Lowell,J.B. | | | |
| TITLE | UCP3: an uncoupling protein homologue expressed preferentially and abundantly in skeletal muscle and brown adipose tissue | | | |
| JOURNAL | Biochem. Biophys. Res. Commun. 235 (1), 79-82 (1997) | | | |
| MEDLINE | 9739440 | | | |
| PUBMED | 9196039 | | | |
| REFERENCE | 2 (bases 1 to 1175) | | | |
| AUTHORS | Vidal-Puig,A., Solanas,G., Grujic,D., Flier,J.S. and Lowell,J.B. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (30-APR-1997) Medicine, Beth Israel Deacones Medical Center, 330 Brookline Ave., Boston, MA 02215, USA | | | |
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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 AUTHORS Gong,D.W., He,Y., Karas,M. and Reitman,M.
 TITLE Uncoupling protein-3 is a mediator of thermogenesis regulated by
 thyroid hormone, beta3-adrenergic agonists, and leptin
 JOURNAL J. Biol. Chem. 272 (39), 24129-24132 (1997)
 MEDLINE 97450925
 PUBMED 9305858
 REFERENCES 2 (bases 1 to 1104)
 AUTHORS Gong,D.-W., He,Y., Karas,M. and Reitman,M.
 TITLE Direct Submission
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 Job time : 4813 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: May 18, 2004, 11:12:25 ; Search time 123 Seconds
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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 7 | 732 | 59.5 | 2782 | 2 | US-09-172-528-1 |
| 8 | 732 | 59.5 | 2782 | 3 | US-09-318-199-1 |
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| 14 | 593.8 | 48.2 | 1777 | 2 | US-08-937-466-5 |
| 15 | 593.8 | 48.2 | 1777 | 2 | US-09-172-528-5 |
| 16 | 593.8 | 48.2 | 1777 | 3 | US-09-318-199-5 |
| 17 | 593.8 | 48.2 | 1777 | 3 | US-09-503-579-5 |
| 18 | 476.6 | 38.7 | 1596 | 2 | US-08-807-861A-38 |
| 19 | 476.6 | 38.7 | 1596 | 3 | US-09-210-681-38 |
| 20 | 476.6 | 38.7 | 1596 | 3 | US-08-946-719A-38 |
| 21 | 476.6 | 38.7 | 1596 | 4 | US-09-547-983-38 |
| 22 | 475.6 | 38.6 | 930 | 4 | US-10-001-051B-1 |
| 23 | 457.2 | 37.1 | 1255 | 1 | US-08-470-868B-38 |
| 24 | 457.2 | 37.1 | 1255 | 1 | US-08-294-522B-38 |
| 25 | 457.2 | 37.1 | 1255 | 2 | US-08-470-868A-38 |
| 26 | 441.8 | 35.9 | 847 | 3 | US-09-142-565-5 |
| 27 | 385.6 | 31.3 | 1205 | 1 | US-08-518-878B-36 |

| | | | | | | |
|----|-------|------|------|---|---------------------|-------------------|
| 28 | 385.6 | 31.3 | 1205 | 1 | US-08-294-522B-37 | Sequence 37, Appl |
| 29 | 385.6 | 31.3 | 1205 | 2 | US-08-807-861A-36 | Sequence 36, Appl |
| 30 | 385.6 | 31.3 | 1205 | 3 | US-08-470-868A-36 | Sequence 36, Appl |
| 31 | 385.6 | 31.3 | 1205 | 3 | US-09-210-681-36 | Sequence 36, Appl |
| 32 | 385.6 | 31.3 | 1205 | 4 | US-08-946-719A-36 | Sequence 36, Appl |
| 33 | 385.6 | 31.3 | 1205 | 4 | US-09-547-983-36 | Sequence 36, Appl |
| 34 | 326.8 | 26.5 | 924 | 4 | US-09-023-655-890 | Sequence 890, App |
| 35 | 254.4 | 20.7 | 512 | 4 | US-09-702-705-1014 | Sequence 1014, Ap |
| 36 | 254.4 | 20.7 | 512 | 4 | US-09-736-457-1014 | Sequence 1014, Ap |
| 37 | 254.4 | 20.7 | 512 | 4 | US-09-614-124B-1014 | Sequence 1014, Ap |
| 38 | 254.4 | 20.7 | 512 | 4 | US-09-671-325-1014 | Sequence 1014, Ap |
| 39 | 201 | 16.3 | 222 | 3 | US-09-142-565-3 | Sequence 3, Appl1 |
| 40 | 171.6 | 13.9 | 309 | 1 | US-08-518-878B-14 | Sequence 14, Appl |
| 41 | 171.6 | 13.9 | 309 | 1 | US-08-294-522B-14 | Sequence 14, Appl |
| 42 | 171.6 | 13.9 | 309 | 2 | US-08-807-861A-14 | Sequence 14, Appl |
| 43 | 171.6 | 13.9 | 309 | 2 | US-08-470-868A-14 | Sequence 14, Appl |
| 44 | 171.6 | 13.9 | 309 | 3 | US-09-210-681-14 | Sequence 14, Appl |
| 45 | 171.6 | 13.9 | 309 | 3 | US-08-946-719A-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-09-808-457-1
Sequence 1, Application US/09808457

Patent No. 6608038
GENERAL INFORMATION:

APPLICANT: Boehringer, Brian
APPLICANT: Caplan, Shari
APPLICANT: Kaleko, Michael
APPLICANT: Connolly, Sheila
APPLICANT: Desai, Urvil
APPLICANT: Sloeber, Eric
TITLE OF INVENTION: Methods and Compositions For Treatment
TITLE OF INVENTION: Of Diabetes and Related Conditions Via Gene Therapy
FILE REFERENCE: 4-31353A/USN
CURRENT APPLICATION NUMBER: US/09/808,457
CURRENT FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: 60/XXX,XXX
PRIORITY FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1231
TYPE: DNA
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: cDNA from clone UCP3L
US-09-808-457-1

Query Match 100.0%; Score 1231; DB 4; Length 1231;
Best Local Similarity 100.0%; Pred. No. 2.8e-307; Indels 0; Gaps 0;
Matches 1231; Conservative 0; Mismatches 0

| | | | |
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| QY | 1 | TCTTGAGATGAGACCCCTAGGAGCCCTGTGCTGCCCTGCGTGGACGACTCAGACC | 60 |
| DB | 1 | TCTTGAGATGAGACCCCTAGGAGCCCTGTGCTGCCCTGCGTGGAGACTCAGAGCC | 60 |
| QY | 61 | CCACCGCTGACTGAAGCCAGGCGCTGTGAGAGAGCTCTCTCTTGAACCTCTCTCGG | 120 |
| DB | 61 | CCACCGCTGACTGAAGCCAGGCGCTGTGAGAGAGCTCTCTCTTGAACCTCTCTCGG | 120 |
| QY | 121 | CCCTAAAGGAGCTGGGAGAGCCCTTCAGAGACTATGTTGAGCTGAAGCTTCAAGCTG | 180 |
| DB | 121 | CCCTAAAGGAGCTGGGAGAGCCCTTCAGAGACTATGTTGAGCTGAAGCTTCAAGCTG | 180 |
| QY | 181 | CCCTCCACATGCTGTGAAGTTCTGTGGGCGAGGACACAGACCTGTGTTGTGACTTC | 240 |
| DB | 181 | CCCTCCACATGCTGTGAAGTTCTGTGGGCGAGGACACAGACCTGTGTTGTGACTTC | 240 |
| QY | 241 | GTTACCTTTGACTGACACAGCCAGAGTCCGCTGTGAGATCCAGGGGAGAACAGGCG | 300 |
| DB | 241 | GTTACCTTTGACTGACACAGCCAGAGTCCGCTGTGAGATCCAGGGGAGAACAGGCG | 300 |

Db 241 GTTACTTTTCATGAGACAGACCAAGGTCCGCTGCAATCCAGGGGAGAACAGGCG 300
 QY 301 GTCCAGACGGCCCGGCTGTCAGATCCGTGGCGTGTGGGACACCATCTGACATGCTG 360
 Db 301 GTCCAGACGGCCCGGCTGTCAGATCCGTGGCGTGTGGGACACCATCTGACATGCTG 360
 QY 361 CGGACTGAGGGTCCCTGACAGCCCTTAACAATGGGCTGTGGCCGGCTGACGGCCAGT 420
 Db 361 CGGACTGAGGGTCCCTGACAGCCCTTAACAATGGGCTGTGGCCGGCTGACGGCCAGT 420
 QY 421 AGCTTGCGCTCCATCCGATCGGCTCTATATGCTCCGTCACAGCAGTGTACACCCCAA 480
 Db 421 AGCTTGCGCTCCATCCGATCGGCTCTATATGCTCCGTCACAGCAGTGTACACCCCAA 480
 QY 481 GGGCGGGAACAATCCAGGCTCACTACCCGGATTTTGGCCGGCTGACCAAGAGGACATG 540
 Db 481 GGGCGGGAACAATCCAGGCTCACTACCCGGATTTTGGCCGGCTGACCAAGAGGACATG 540
 QY 541 GCGGTGACCTGTGCCCAAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGATACAC 600
 Db 541 GCGGTGACCTGTGCCCAAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGATACAC 600
 QY 601 CTGCGGCAATCCAGAGGAGCAAGAAATACAGCGGACATATGAGCCCTACAGAACATC 660
 Db 601 CTGCGGCAATCCAGAGGAGCAAGAAATACAGCGGACATATGAGCCCTACAGAACATC 660
 QY 661 GCCAGAGGAGAGAGTCAAGGAGCTGTGTGAAGAACTTTGCCCAACATCATAGAGAT 720
 Db 661 GCCAGAGGAGAGAGTCAAGGAGCTGTGTGAAGAACTTTGCCCAACATCATAGAGAT 720
 QY 721 GCTATCTGTAATGCTGTGAGGTGTGATCAAGATCTTCAAGAGAGAGTGTCTGAC 780
 Db 721 GCTATCTGTAATGCTGTGAGGTGTGATCAAGATCTTCAAGAGAGAGTGTCTGAC 780
 QY 781 TACCACTGCTCACTGACAACTTCCCTGACCTTTGTCTGCTGTTGGAGACCGGCTTC 840
 Db 781 TACCACTGCTCACTGACAACTTCCCTGACCTTTGTCTGCTGTTGGAGACCGGCTTC 840
 QY 841 TGTGCAACAGTGTGGCTCCCGGTGAGCTGTGTGAAGACCGGATATGAACTCACT 900
 Db 841 TGTGCAACAGTGTGGCTCCCGGTGAGCTGTGTGAAGACCGGATATGAACTCACT 900
 QY 901 CCAAGCCAGTACTTCAAGCCCTCTGATGTATGATTAAGATGTGTGAGAGAGGAGG 960
 Db 901 CCAAGCCAGTACTTCAAGCCCTCTGATGTATGATTAAGATGTGTGAGAGAGGAGG 960
 QY 961 AAGCCTTCTAAGAGGATTTTACACCTCTCTTTTGGCTTTGGAGTCCCTGAACTGTG 1020
 Db 961 AAGCCTTCTAAGAGGATTTTACACCTCTCTTTTGGCTTTGGAGTCCCTGAACTGTG 1020
 QY 1021 ATGTCTGTAACTATGAGAGCTGAAAGGGGCTGTGATGAAGTCAAGATGTTACGGGA 1080
 Db 1021 ATGTCTGTAACTATGAGAGCTGAAAGGGGCTGTGATGAAGTCAAGATGTTACGGGA 1080
 QY 1081 TCACGCTTTGAAACAAGAGGCACTGGTACTAAGCTGTCCGAAACAGATTAA 1140
 Db 1081 TCACGCTTTGAAACAAGAGGCACTGGTACTAAGCTGTCCGAAACAGATTAA 1140
 QY 1141 AATGGAAGAAACGGTGCATCCAGCAACATGGAACAGACCCCAACATGTTTACAGA 1200
 Db 1141 AATGGAAGAAACGGTGCATCCAGCAACATGGAACAGACCCCAACATGTTTACAGA 1200
 QY 1201 CTGTTGTTACTGTTGTGATTTCAAGAAAC 1231
 Db 1201 CTGTTGTTACTGTTGTGATTTCAAGAAAC 1231

RESULT 2
 US-09-423-410-3
 ; Sequence 3, Application US/09423410
 ; Patent No. 6620594
 ; GENERAL INFORMATION:
 ; APPLICANT: Giacobino, Jean-Paul

; APPLICANT: Muzzin, Patrick
 ; APPLICANT: Bosc, Olivier
 ; TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3
 ; FILE REFERENCE: 4-30353/A
 ; CURRENT APPLICATION NUMBER: US/09/423,410
 ; EARLIER FILING DATE: 1998-11-04
 ; EARLIER APPLICATION NUMBER: PCT/EP98/02645
 ; EARLIER FILING DATE: 1998-05-05
 ; EARLIER APPLICATION NUMBER: 1072/97
 ; EARLIER FILING DATE: 1997-05-07
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1231
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURES:
 ; OTHER INFORMATION: Description of Unknown Organism: cDNA from clone
 ; OTHER INFORMATION: UCP3L
 ; US-09-423-410-3

Query Match 100.0%; Score 1231; DB 4; Length 1231;
 Best Local Similarity 100.0%; Pred. No. 2,8e-307;
 Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGGAGTGAAGCCCTTAGGAGCCCTGTGCTGCTCCCTGCGTGGCAGACTCAAGCC 60
 Db 1 TCTGGAGTGAAGCCCTTAGGAGCCCTGTGCTGCTCCCTGCGTGGCAGACTCAAGCC 60
 QY 61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGAGACCTCTCTCTTGAACCTCTCTGG 120
 Db 61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGAGACCTCTCTCTTGAACCTCTCTGG 120
 QY 121 CCTTAAAGGAGCTGGGAGAGACCTTTCAGAGCTATGTTGATCTGAAGCTTTCAGAGCTG 180
 Db 121 CCTTAAAGGAGCTGGGAGAGACCTTTCAGAGCTATGTTGATCTGAAGCTTTCAGAGCTG 180
 QY 181 CCTCCACATGCTGTGAAGTCTGTGGGGAGGAGCAAGAGCTGTGTTGGCTGACCTC 240
 Db 181 CCTCCACATGCTGTGAAGTCTGTGGGGAGGAGCAAGAGCTGTGTTGGCTGACCTC 240
 QY 241 GTTACTTTTCACTGAGACAGCCCAAGGTCGCTGACATCCAGGGGAGAACAGGCG 300
 Db 241 GTTACTTTTCACTGAGACAGCCCAAGGTCGCTGACATCCAGGGGAGAACAGGCG 300
 QY 301 GTCCAGACGGCCCGGCTGTGAGTACCGTGTGCTGTGGGACCATCTGACATGCTG 360
 Db 301 GTCCAGACGGCCCGGCTGTGAGTACCGTGTGCTGTGGGACCATCTGACATGCTG 360
 QY 361 CGGACTGAGGGTCCCTGCAAGCCCTTAACAATGGGCTGTGGCCGGCTGACGGCCAGATG 420
 Db 361 CGGACTGAGGGTCCCTGCAAGCCCTTAACAATGGGCTGTGGCCGGCTGACGGCCAGATG 420
 QY 421 AGCTTGCGCTCCATCCGATCGGCTCTATATGCTCCGTCACAGCAGTGTACACCCCAA 480
 Db 421 AGCTTGCGCTCCATCCGATCGGCTCTATATGCTCCGTCACAGCAGTGTACACCCCAA 480
 QY 481 GGGCGGGAACAATCCAGGCTCACTACCCGGATTTTGGCCGGCTGACCAAGAGGACATG 540
 Db 481 GGGCGGGAACAATCCAGGCTCACTACCCGGATTTTGGCCGGCTGACCAAGAGGACATG 540
 QY 541 GCGGTGACCTGTGCCCAAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGATACAC 600
 Db 541 GCGGTGACCTGTGCCCAAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGATACAC 600
 QY 601 CTGCGGCAATCCAGAGGAGCAAGAAATACAGCGGACATATGAGCCCTACAGAACATC 660
 Db 601 CTGCGGCAATCCAGAGGAGCAAGAAATACAGCGGACATATGAGCCCTACAGAACATC 660
 QY 661 GCCAGAGGAGAGAGTCAAGGAGCTGTGTGAAGAACTTTGCCCAACATCATAGAGAT 720
 Db 661 GCCAGAGGAGAGAGTCAAGGAGCTGTGTGAAGAACTTTGCCCAACATCATAGAGAT 720

| | | | |
|----|-----|--|-----|
| Qy | 601 | CTGCGGCACATCCAGAGAGCGGACAGAAATAACAGCGGGACCTATAGACGCTACAGAACATC | 666 |
| Db | 601 | CTGCGGCACATCCAGAGAGCGACAGAAATAACAGCGGGACCTATAGACGCTACAGAACATC | 666 |
| Qy | 661 | GCCAGGGAGAGAAAGAGTCAAGGGGCTGTGGAAAGAACTTTGCCCAATCATATAGGAAT | 720 |
| Db | 661 | GCCAGGGAGAGAAAGAGTCAAGGGGCTGTGGAAAGAACTTTGCCCAATCATATAGGAAT | 720 |
| Qy | 721 | GCTATCGTCAACTGTGTCTGAGGTGTGAACCTACGACATCTCAAGAGAAAGCTCTGAC | 788 |
| Db | 721 | GCTATCGTCAACTGTGTCTGAGGTGTGAACCTACGACATCTCAAGAGAAAGCTCTGAC | 788 |
| Qy | 781 | TACCACTGTCTACTGACAACTTCCCCCGCCACTTGTCTGTCTGTGAGCCGGCTTC | 848 |
| Db | 781 | TACCACTGTCTACTGACAACTTCCCCCGCCACTTGTCTGTCTGTGAGCCGGCTTC | 848 |
| Qy | 841 | TGTGCCACAGTGTGGCCCTCCCGGTGACGCGTGGAAGACCCGGTATATGAACTCACT | 900 |
| Db | 841 | TGTGCCACAGTGTGGCCCTCCCGGTGACGCGTGGAAGACCCGGTATATGAACTCACT | 900 |
| Qy | 901 | CCAGGCCAAGTACTTCAAGCCCCCTCGACTGTATGATTAAGATGTGTGCCCAAGAGGGCCCC | 960 |
| Db | 901 | CCAGGCCAAGTACTTCAAGCCCCCTCGACTGTATGATTAAGATGTGTGCCCAAGAGGGCCCC | 960 |
| Qy | 961 | ACAAGCTTCTACAAGGGATTTACACCCCTCT | 991 |
| Db | 961 | ACAAGCTTCTACAAGGGGTGAGCCTCTCTCT | 991 |

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RESULT 5
US-09-423-410-5
; Sequence 5, Application US/09423410
; Patent No. 6620594
; GENERAL INFORMATION:
; APPLICANT: Giacobino, Jean-Paul
; APPLICANT: Muzzin, Patrick
; APPLICANT: Boss, Olivier
; TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3
; FILE REFERENCE: 4-30353/A
; CURRENT APPLICATION NUMBER: US/09/423,410
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: PCT/Ep98/02645
; EARLIER FILING DATE: 1998-05-05
; EARLIER APPLICATION NUMBER: 1072/97
; EARLIER FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: cDNA from clone
; OTHER INFORMATION: UCP3S
US-09-423-410-5

Query Match          79.7%; Score 981.4; DB 4; Length 1132;
Best Local Similarity 99.4%; Pred. No. 4.5e-243;
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0

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1  TCCTGGATGAGCCCTTAGGGAGCCCTGTGTGCTGCCCTTCCCTGGACAGACTCAGAGCC 60
1  CCACCGCTGCACTGAAGCCCAAGGGCTGTGAGACACCTCTCTCTTTGACCTCTCTCGG 120
121 CCTTAAAGGAGCTGGGCAAGAGCTTCCAGAGCTATAGTTGAAGTAAAGCTTCAAGAGTG 180
121 CCTTAAAGGAGCTGGGCAAGAGCTTCCAGAGCTATAGTTGAAGTAAAGCTTCAAGAGTG 180

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QY 181 CCTCCACACATGGCTGTGAAGTTCTGCGGGGAGAGACAGACGCTTTTGTGACCTC 240
 Db 181 CCTCCACACATGGCTGTGAAGTTCTGCGGGGAGAGACAGACGCTTTTGTGACCTC 240
 QY 241 GTTACCTTTCATCGACACAGCCAAAGTCCGCTGACATCCAGGGGAGAACCAAGCG 300
 Db 241 GTTACCTTTCATCGACACAGCCAAAGTCCGCTGACATCCAGGGGAGAACCAAGCG 300
 QY 301 GTCCAGACGCGCCGCTGTGACATCGGTGGCTGTGGGACCATCTTACCATGTGTG 360
 Db 301 GTCCAGACGCGCCGCTGTGACATCGGTGGCTGTGGGACCATCTTACCATGTGTG 360
 QY 361 CGGACTGAGGGTCCCTGACGCCCCCTACAAATGGGCTGTGGCGGCTTGACGCGCAGATG 420
 Db 361 CGGACTGAGGGTCCCTGACGCCCCCTACAAATGGGCTGTGGCGGCTTGACGCGCAGATG 420
 QY 421 AGCTTGCCTCCATCCGATCGGCTCTATGATCCGCTCAAGAGGTGTACACCCCAAA 480
 Db 421 AGCTTGCCTCCATCCGATCGGCTCTATGATCCGCTCAAGAGGTGTACACCCCAAA 480
 QY 481 GCGCGGACACTCCAGCTCACTACCCGATTTTGGCGGCTGACACAGAGCCATG 540
 Db 481 GCGCGGACACTCCAGCTCACTACCCGATTTTGGCGGCTGACACAGAGCCATG 540
 QY 541 GGGGTGACCTGTGCCCCAGCCCAAGATGTGTGAAGTCCGATTTTCAAGGCGCAGATAC 600
 Db 541 GGGGTGACCTGTGCCCCAGCCCAAGATGTGTGAAGTCCGATTTTCAAGGCGCAGATAC 600
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 Db 601 CTCGGGCTCATCCAGAGGACAGAAATACAGCGGAGCTATGAGCCCTTACAGAACATC 660
 QY 661 GCCAGGAGGAAAGAGTCAAGGGGCTGTGAAAGAACTTTGCGCAACATCATAGGAAT 720
 Db 661 GCCAGGAGGAAAGAGTCAAGGGGCTGTGAAAGAACTTTGCGCAACATCATAGGAAT 720
 QY 721 GCTATGTGCACTGTCTGTGAGGTGTGACCTTACAGATCTTCAAGAGAAAGTGTGAGC 780
 Db 721 GCTATGTGCACTGTCTGTGAGGTGTGACCTTACAGATCTTCAAGAGAAAGTGTGAGC 780
 QY 781 TACCACTTGTCACTACAACTTCCCTGCACTTTGTCTGTGAGCGGCTTC 840
 Db 781 TACCACTTGTCACTACAACTTCCCTGCACTTTGTCTGTGAGCGGCTTC 840
 QY 841 TGTGCCACAGTGTGCTCTCCCGGTGACGTGTGAAAGACCCGATATGAACTACCT 900
 Db 841 TGTGCCACAGTGTGCTCTCCCGGTGACGTGTGAAAGACCCGATATGAACTACCT 900
 QY 901 CCAAGGCACTATCTTCAAGCCCCCTGCACTGTATGATAAAGATGTGAGCCAGAGGGGCGCC 960
 Db 901 CCAAGGCACTATCTTCAAGCCCCCTGCACTGTATGATAAAGATGTGAGCCAGAGGGGCGCC 960
 QY 961 ACAGCCTTCTACAAAGGATTTTACACCTCTCT 991
 Db 961 ACAGCCTTCTACAAAGGATTTTACACCTCTCT 991

RESULT 6

US-08-937-466-1

Sequence 1, Application US/08937466

Patent No. 5846779

GENERAL INFORMATION:

APPLICANT: Zhang, Ning

APPLICANT: Amaral, M. Catherine

APPLICANT: Chen, Jin-Long

TITLE OF INVENTION: UCP3 Genes

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,466
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2782 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-937-466-1

Query Match 59.5%; Score 732; DB 2; Length 2782;
 Best Local Similarity 81.1%; Pred. No. 9e-179;
 Matches 904; Conservative 0; Mismatches 195; Indels 15; Gaps 4;
 QY 4 TGGGATGAGACCTTGAAGGAGCCCTGTGTGCTGCCCCCTGCGGTGAGAGACTCAAGCCCA 63
 Db 93 TGAAGTGAACCTTGAAGGAGGCTGTGCACT ACCCACTTGTGTGAGAGCAAGCTTCC 151
 QY 64 CGCTGCACTGAAGCCAGGCGGTGTGAGCAAGCTTCTCTTGAACCTTCTGAGCC 123
 Db 152 TCCTGAACTGAAGCAAAAGATTGCCAGGCAAGCTTCTCTGAGCTCAATAGGACAG 211
 QY 124 TAAAGGACTGGGCAAGGCTTCCAGAGTATGTGTGACTGAAGCTTCAAGCTTCC 183
 Db 212 AAAGGAAACAGGCGCAATTC--CGGAGCAATGTGTGACTTCAAGCTTCAAGAGTCC 269
 QY 184 CCACACAGCTGTGAAGTTCCTGGGGGAGGACAGAGCTGTTTGTCTGACTGCTT 243
 Db 270 CCACACAGCTGTGAAGTTCCTGGGGGAGGACAGAGCTGTTTGTCTGACTGCTT 329
 QY 244 ACCTTTCACTGAGACACAGCAAGTCCGCTGCAAGTCCAGGGGAGAAACAGGCGTC 303
 Db 330 ACTTTTCCCTGAGACAGCGCAAGTCCGCTGCAAGTCCAGGGGAGAAACAGGCGTC 389
 QY 304 CAGACGCGCCGCTGTGAGTACCGTGTGCTGTGGCACTCTTACATGTGTGCGG 363
 Db 390 CAGA-----GCGTGAAGTACCGGCTGTGTGCTGTGGCACTCTTACATGTGTGCGG 440
 QY 364 ACTGAGGGTCCCTGACGCCCCCTACAAATGGGCTGTGGCGGCGCTGACGCGCAGATGAGC 423
 Db 441 ACAGAGGGTCCCTGACGCCCCCTACAGGAGTGTGTGCTGTGGCGGCGCTGACGCGCAGATGAGT 500
 QY 424 TTGCTTCATCCGATCGGCTCTATGACTCGTCAAGAGTGTACACCCCAAGGC 483
 Db 501 TTGCTTCATCCGATCGGCTCTATGACTCGTCAAGAGTGTACACCCCAAGGC 560
 QY 484 GGGAGACATCCAGCTCACTACCGGATTTTGGCGGCTGCAACAGAGGCTATGGG 543
 Db 561 GGGAGACATCCAGCTCGCTCCCATCAAGATTTGCGAGCTGACGACAGAGGCTATGGG 620
 QY 544 GTGACCTGTGCCAGGCCACAGATGTGTGAAGTCCGATTTTCAAGGCGCAGATACCTC 603
 Db 621 GTGACCTGTGCCAGGCCACAGATGTGTGAAGTCCGATTTTCAAGGCGCAGATACCTC 680
 QY 604 GGGCCATCCAGAGGACAGAAATACAGCGGAGCTATGAGCGCTTACAGAACATGCGC 663
 Db 681 GG---AAGTGAAGAGAGAAATACAGAGGAGCTATGATGTCTTACAGAACATGCGC 737

QY 664 AGGAGAGAGAGTCAAGGAGCTGTGAGAAAGACTTGGCCCAATCATGAGAAATGCT 723
DB 738 AGGAGAGAGAGTCAAGGAGCTGTGAGAAAGACTTGGCCCAATCATGAGAAATGCT 797
QY 724 ATGCTCACTGTGTGAGAGTGTGAGTCACTGAGCACTCTCAAGAGAAAGCTGTGACTAC 783
DB 798 ATTGTCACTGTGTGAGAGTGTGAGTCACTGAGCACTCTCAAGAGAAAGTGTGTGAGTCT 857
QY 784 CACTGTCTCACTGAGCACTTCCCTGCGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
DB 858 CACTGT 917
QY 844 GCGCAGT 903
DB 918 GCGCAGT 977
QY 904 GCGCAGT 963
DB 978 GCGCAGT 1037
QY 964 GCGTCTTCAAGAGATTTTACACCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023
DB 1038 GCGTCTTCAAGAGATTTTGT 1097
QY 1024 TTGCTTAACCTTAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
DB 1098 TTGCTTAACCTTAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1157
QY 1084 CCGTTTGAACAG 1117
DB 1158 CCGTTTGAACAG 1191

RESULT 7

US-09-172-528-1

Sequence 1, Application US/09172528

Patent No. 5952469

GENERAL INFORMATION:

APPLICANT: Zhang, Ning

APPLICANT: Amarel, M. Catherine

APPLICANT: Chen, Jin-Long

TITLE OF INVENTION: UCP3 Gene

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/172,528

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/937,466

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-009

TELEPHONE: (650) 343-4341

TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2782 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-172-528-1

Query Match 59.5%; Score 732; DB 2; Length 2782;
Best Local Similarity 81.1%; Pred. No. 9e-179;
Matches 904; Conservative 0; Mismatches 195; Indels 15; Gaps 4;

QY 4 TGGAGTGGAGCCCTTGAAGAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 63
DB 93 TGGAGTGGAGCCCTTGAAGAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 151
QY 64 CCGCTGCACTGAGAGCCAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 152 TCCCTGAACTGAAAG 211
QY 124 TAAAGGAGCTGGGAG 183
DB 212 AAAG 269
QY 184 CCGCAG 243
DB 270 CCGCAG 329
QY 244 ACCCTTCACTGAG 303
DB 330 ACTTTTCCCTGAG 389
QY 304 CAG 363
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DB 501 TTGCTCTCATTCGAG 560
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| QY | 1084 | CCGTTTGAACAAAGCAAGAGGCCTAGTAGC | 1117 |
| Db | 1158 | CCGTTTGAACAAAGCAAGAGGCCTAGTAAC | 1191 |

RESULT 8

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US-09-318-199-1
Sequence 1, Application US/09318199
Patent No. 6025469
GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/318,199
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2782 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-318-199-1

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; Sequence 1, Application US/09503579
; Patent No. 6248561
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning


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; GENERAL INFORMATION:
; APPLICANT: Zhang, Ning
; APPLICANT: Amarel, M. Catherine
; APPLICANT: Chen, Jin-Long
; TITLE OF INVENTION: UCP3 Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,579
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,466

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; TELEPHONE/DOCKET NUMBER: T97-009
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 1145.4 | 93.0 | 1192 | 9 | US-09-734-134-1 |
| 4 | 981.4 | 79.7 | 1132 | 9 | US-09-808-457-3 |
| 5 | 981.4 | 79.7 | 1132 | 10 | US-09-823-866A-5 |
| 6 | 490 | 39.8 | 1575 | 9 | US-09-917-800A-1679 |
| 7 | 490 | 39.8 | 1575 | 12 | US-10-152-319A-1731 |
| 8 | 476.6 | 38.7 | 1505 | 10 | US-09-823-866A-3 |
| 9 | 476.6 | 38.7 | 1612 | 15 | US-10-265-689-13 |
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| 11 | 476.6 | 38.7 | 1646 | 16 | US-10-159-563-344 |
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| 43 | 162 | 13.2 | 318 | 13 | US-10-283-017-1376 | Sequence 1376, App |
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ALIGNMENTS

RESULT 1
US-09-808-457-1
X Sequence 1, Application US/09808457 056608038

Patent No. US2002065239A1

GENERAL INFORMATION:
APPLICANT: Boettcher, Brian
APPLICANT: Kaplan, Shari
APPLICANT: Kaleko, Michael
APPLICANT: Connolly, Shella
APPLICANT: Desai, Dru
APPLICANT: Slossberg, Eric
TITLE OF INVENTION: Methods and Compositions For Treatment
of Diabetes and Related Conditions Via Gene Therapy
FILE REFERENCE: 4-31353A/USN
CURRENT APPLICATION NUMBER: US/09/808,457
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/XXX,XXX
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1231
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: cDNA from clone UCP3L
US-09-808-457-1

Query Match 100.0%; Score 1231; DB 9; Length 1231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 721 GCTATGCTCACTGTGCTGAGGTGTGACTGACATCTTCAAGAGAACTGTGAG 780
 Db 721 GCTATGCTCACTGTGCTGAGGTGTGACTGACATCTTCAAGAGAACTGTGAG 780
 Qy 781 TACCACTGCTGACATCACTTCCCTGCTGCACTTGTCTGCTTGGAGCGGCTTC 840
 Db 781 TACCACTGCTGACATCACTTCCCTGCTGCACTTGTCTGCTTGGAGCGGCTTC 840
 Qy 841 TGTGACACAGTGTGCTGCTGCGGTGAGAGTGTGAGAGCCGGATATAGACTACCT 900
 Db 841 TGTGACACAGTGTGCTGCTGCGGTGAGAGTGTGAGAGCCGGATATAGACTACCT 900
 Qy 901 CCAAGGCAAGTCTTCAAGCCCTGCACTGTATATTAAGATGTGTGCGCCAGGAGG 960
 Db 901 CCAAGGCAAGTCTTCAAGCCCTGCACTGTATATTAAGATGTGTGCGCCAGGAGG 960
 Qy 961 ACAGGCTTCTTCAAGAGGATTAACCTCTTGTGTGGTGGAGTCCGGAACGTGTG 1020
 Db 961 ACAGGCTTCTTCAAGAGGATTAACCTCTTGTGTGGTGGAGTCCGGAACGTGTG 1020
 Qy 1021 ATGTGCTTATCTATGAGCAGTGAACCGGCTCTGATGAAGTTCAGATGTTACGGGA 1080
 Db 1021 ATGTGCTTATCTATGAGCAGTGAACCGGCTCTGATGAAGTTCAGATGTTACGGGA 1080
 Qy 1081 TCAACGTTTGAACAGAGAGAGGCACTGTGATTAAGTGTCCGAAACAGATTAG 1140
 Db 1081 TCAACGTTTGAACAGAGAGAGGCACTGTGATTAAGTGTGTCCGAAACAGATTAG 1140
 Qy 1141 AATGAGAGAGAGAGGCTGATCCAGCAGATGAGCAGAGCCACATGTTTACGAA 1200

Db 1141 AATGAGAGAGAGAGGCTGATCCAGCAGATGAGCAGAGCCACATGTTTACGAA 1200
 Qy 1201 CTGTGTTTACTGTGTGCTGATTCAGAGAAC 1231
 Db 1201 CTGTGTTTACTGTGTGCTGATTCAGAGAAC 1231
 RESULT 2
 US-09-826-507-1
 ; Sequence 1, Application US/09826507
 ; Patent No. US2002004492A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee James Beasley
 ; APPLICANT: John Christopher Clapham
 ; APPLICANT: Robert James Godden
 ; TITLE OF INVENTION: NEW USE
 ; FILE REFERENCE: GH-30009-C1
 ; CURRENT APPLICATION NUMBER: US/09/826,507
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR FILING DATE: 1999-05-17
 ; PRIOR APPLICATION NUMBER: 9814926.3
 ; PRIOR FILING DATE: 1998-07-09
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1193
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS
 ; US-09-826-507-1

Query Match 93.1%; Score 1146.4; DB 9; Length 1193;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCTGGAGTGAAGGCTTGAAGGAGCCCTGTGCTGCGCTGCGGAGAGACTCAGAGC 60
 Db 46 TCCTGGAGTGAAGGCTTGAAGGAGCCCTGTGCTGCGCTGCGGAGAGACTCAGAGC 105
 Qy 61 CCACGCTGCTGACTGAAGCCAGGCGCTGTGAGAGAGCTCTCTCTTGGAGCTCTCTCG 120
 Db 106 CCACGCTGCTGACTGAAGCCAGGCGCTGTGAGAGAGCTCTCTCTTGGAGCTCTCTCG 165
 Qy 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGACTATGTGTGAGCTGAAGCTTCAAGCTG 180
 Db 166 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGACTATGTGTGAGCTGAAGCTTCAAGCTG 225
 Qy 181 CCTCCACCATGCTGTGAGAGTCTCTGAGGAGGAGCAGAGAGCTGTTTGTGACTCTC 240
 Db 226 CCTCCACCATGCTGTGAGAGTCTCTGAGGAGGAGCAGAGAGCTGTTTGTGACTCTC 285
 Qy 241 GTTACTCTTCCAGTGGAGCAGGCTCAAGGCTGCTGCAATCAAGGGGAGAGAACAGGG 300
 Db 286 GTTACTCTTCCAGTGGAGCAGGCTCAAGGCTGCTGCAATCAAGGGGAGAGAACAGGG 345
 Qy 301 GTTCAAGCGGCGCGCTGCTGAGAGTACCGTGGCGGTGTGGGAGCCTTGAACATGTG 360
 Db 346 GTTCAAGCGGCGCGCTGCTGAGAGTACCGTGGCGGTGTGGGAGCCTTGAACATGTG 405
 Qy 361 CGGACTGAGGGTCTCTGAGGCTTCAATGAGGCTGTGGCGGCTGAGCGGAGATG 420
 Db 406 CGGACTGAGGGTCTCTGAGGCTTCAATGAGGCTGTGGCGGCTGAGCGGAGATG 465
 Qy 421 AGCTTGTGCTTCCATCGGAGTCCGCTCTATGACTCCGCTCAAGAGGTTTACACCCCA 480
 Db 466 AGCTTGTGCTTCCATCGGAGTCCGCTCTATGACTCCGCTCAAGAGGTTTACACCCCA 525
 Qy 481 GCGCGGAGCAATCCAGGCTCACTACCGGATTTTGGCGGCTGACACAGAGGAGC 540
 Db 526 GCGCGGAGCAATCCAGGCTCACTACCGGATTTTGGCGGCTGACACAGAGGAGC 585
 Qy 541 GCGGTAAGCTGTGCGCCAGCCACAGATGTGTGAGAGTCCGATTTTCAGGCTCAGATC 600


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Db      1066 ATGTCGTAACCTATGACAGCTGAAGCGGCGCTGATGAAGTCCAGATGTTACGGGAA 1125
Qy      1081 TCACCGTTTGAACAAGACAAGAGGCCACTGTAGTACGTATCCGAAACAGATTAG 1140
Db      1126 TCACCGTTTGAACAAGACAAGAGGCCACTGTAGTACGTATCCGAAACAGATTAG 1185
Qy      1141 AATGGA 1147
Db      1186 AATGGA 1192

RESULT 4
US-09-808-457-3
; Sequence 3, Application US/09808457
; Patent No. US20020065239A1
; GENERAL INFORMATION:
; APPLICANT: Boeitcher, Brian
; APPLICANT: Caplan, Shari
; APPLICANT: Kaleko, Michael
; APPLICANT: Connelly, Sheila
; APPLICANT: Desai, Urv
; APPLICANT: Slobberg, Eric
; TITLE OF INVENTION: Methods and Compositions For Treatment
; TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy
; FILE REFERENCE: 4-31353A/USN
; CURRENT APPLICATION NUMBER: US/09/808,457
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/XXX,XXX
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: cDNA from clone UCP35
US-09-808-457-3

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Query Match      79.7%; Score 981.4; DB 9; Length 1132;
Best Local Similarity 99.4%; Pred. No. 1.1e-277;
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TCCTGGATGAGACCTTGAAGAGCCCTGTGCTGCCCCCTGGGCAAGACTCAAGCC 60
Db      1 TCCTGGATGAGACCTTGAAGAGCCCTGTGCTGCCCCCTGGGCAAGACTCAAGCC 60
Qy      61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTTGAACCTCTCTCG 120
Db      61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTTGAACCTCTCTCG 120
Qy      121 CCTTAAAGGAGCTGGGCAAGAGCTTCCAGAGACTATAGTGTGAAGAGCTTCAAGCG 180
Db      121 CCTTAAAGGAGCTGGGCAAGAGCTTCCAGAGACTATAGTGTGAAGAGCTTCAAGCG 180
Qy      122 CCTTAAAGGAGCTGGGCAAGAGCTTCCAGAGACTATAGTGTGAAGAGCTTCAAGCG 180
Db      122 CCTTAAAGGAGCTGGGCAAGAGCTTCCAGAGACTATAGTGTGAAGAGCTTCAAGCG 180
Qy      181 CCTCCACCATGAGCTGTGAAGTTCCTGAGGAGAGGAGCAAGAGCTGTTTGTGACCTC 240
Db      181 CCTCCACCATGAGCTGTGAAGTTCCTGAGGAGAGGAGCAAGAGCTGTTTGTGACCTC 240
Qy      241 GTTACCTTTCACCTGAGCAAGCAAGGTCCTGCTGCAATCCAGGGGAGAAACAGGCG 300
Db      241 GTTACCTTTCACCTGAGCAAGCAAGGTCCTGCTGCAATCCAGGGGAGAAACAGGCG 300
Qy      301 GTTCAAGAGCGCGCGCTGCTGAGTACCGTGGGCTGTGGGCAACATCCGACCAATGGT 360
Db      301 GTTCAAGAGCGCGCGCTGCTGAGTACCGTGGGCTGTGGGCAACATCCGACCAATGGT 360
Qy      361 CGGACTGAGAGGTCCTGCTGAGCGCCCTTCAATGGGCTGTGGGCGGCTGCAAGCGCCAGAT 420
Db      361 CGGACTGAGAGGTCCTGCTGAGCGCCCTTCAATGGGCTGTGGGCGGCTGCAAGCGCCAGAT 420
Qy      421 AGCTTGCCCTCCATCCGCAATGGGCTGTATGACTCCGTCAAGAGGTATACACCCCAAA 480

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Db      421 AGCTTGCCCTCCATCCGCAATGGGCTGTATGACTCCGTCAAGAGGTATACACCCCAAA 480
Qy      481 GGGCGGACAATCTCAGGCTCACTACCCGAGATTTTGGCGGGCTGCACCAAGAGCCATG 540
Db      481 GGGCGGACAATCTCAGGCTCACTACCCGAGATTTTGGCGGGCTGCACCAAGAGCCATG 540
Qy      541 GGGGTACCTGTGGCCAGCCCAAGATGTGTGAAGTTCGATTTTCAAGCCAGATAC 600
Db      541 GGGGTACCTGTGGCCAGCCCAAGATGTGTGAAGTTCGATTTTCAAGCCAGATAC 600
Qy      601 CTGGGCGCATCCAGAGGAGCAAGAAATACAGCGGAGCTATGAGCGCTTACAGAACATC 660
Db      601 CTGGGCGCATCCAGAGGAGCAAGAAATACAGCGGAGCTATGAGCGCTTACAGAACATC 660
Qy      661 GCCAGAGAGAGAGTCAAGGCGCTGTGAAGAGAACTTTGCCCAATCATAGAGAT 720
Db      661 GCCAGAGAGAGAGTCAAGGCGCTGTGAAGAGAACTTTGCCCAATCATAGAGAT 720
Qy      721 GCTATCGTCAACTGTGCTGAGAGTGTGACTTACGACATCTTCAAGAGAACTGTGAC 780
Db      721 GCTATCGTCAACTGTGCTGAGAGTGTGACTTACGACATCTTCAAGAGAACTGTGAC 780
Qy      781 TACCACTGCTCAGTGAACAATTGCCCTGCACTTGTCTGCTTGAAGCGGCTTC 840
Db      781 TACCACTGCTCAGTGAACAATTGCCCTGCACTTGTCTGCTTGAAGCGGCTTC 840
Qy      841 TGTGCAAGAGTGTGCTCCCGGCTGAGCGTGTGAAGAGCCGGTATATGAACTCACT 900
Db      841 TGTGCAAGAGTGTGCTCCCGGCTGAGCGTGTGAAGAGCCGGTATATGAACTCACT 900
Qy      901 CCAGGCGAGTACTTCAAGGAGTTTACACCCCTCT 991
Db      901 CCAGGCGAGTACTTCAAGGAGTTTACACCCCTCT 991
Qy      961 ACAGCTTCTACAGGAGTTTACACCCCTCT 991
Db      961 ACAGCTTCTACAGGAGTTTACACCCCTCT 991

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RESULT 5
US-09-823-886A-5
; Sequence 5, Application US/09823886A
; Publication No. US20030150022A1
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha
; APPLICANT: Berry-Lowe, Sandra
; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
; FILE REFERENCE: C1102/7002
; CURRENT APPLICATION NUMBER: US/09/823,886A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,533
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-886A-5

Query Match      79.7%; Score 981.4; DB 10; Length 1132;
Best Local Similarity 99.4%; Pred. No. 1.1e-277;
Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 TCCTGGATGAGACCTTGAAGAGCCCTGTGCTGCCCCCTGGGCAAGACTCAAGCC 60
Db      1 TCCTGGATGAGACCTTGAAGAGCCCTGTGCTGCCCCCTGGGCAAGACTCAAGCC 60
Qy      61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTTGAACCTCTCTCG 120
Db      61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTTGAACCTCTCTCG 120

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QY 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 180
 DB 121 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 180
 QY 181 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 240
 DB 181 CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 240
 QY 241 GTTACCTTTCATGAGCAAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 300
 DB 241 GTTACCTTTCATGAGCAAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 300
 QY 301 GTTACCTTTCATGAGCAAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 360
 DB 301 GTTACCTTTCATGAGCAAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 360
 QY 361 CGGAGTGAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 420
 DB 361 CGGAGTGAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 420
 QY 421 AGCTTGCCTTCATGAGCAAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 480
 DB 421 AGCTTGCCTTCATGAGCAAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 480
 QY 481 GGGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 540
 DB 481 GGGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 540
 QY 541 GGGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 600
 DB 541 GGGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 600
 QY 601 CTGCGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 660
 DB 601 CTGCGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 660
 QY 661 GCGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 720
 DB 661 GCGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 720
 QY 721 GCGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 780
 DB 721 GCGGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 780
 QY 781 TACCACTGCTCACTGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 840
 DB 781 TACCACTGCTCACTGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 840
 QY 841 TGTGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 900
 DB 841 TGTGCGGAGCAACTCCAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 900
 QY 901 CGGAGTGAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 960
 DB 901 CGGAGTGAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 960
 QY 961 ACAGCTTTCATGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 991
 DB 961 ACAGCTTTCATGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 991

RESULT 6

US-09-917-800A-1679
 Sequence 1679, Application US/09917800A
 Patent No. US20020119462A1
 GENERAL INFORMATION:
 APPLICANT: Mendick, Donna
 APPLICANT: Porter, Mark
 APPLICANT: Johnson, Kory
 APPLICANT: Castle, Arthur
 APPLICANT: Elashoff, Michael
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US/09/917,800A
 PRIOR FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/222,880
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/290,029
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/290,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/292,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/295,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/297,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/298,884
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 1679
 LENGTH: 1575
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_019354
 US-09-917-800A-1679

Query Match 39.8%; Score 490; DB 9; Length 1575;
 Best Local Similarity 71.3%; Pred. No. 2,6e-133;
 Matches 694; Conservative 0; Mismatches 265; Indels 15; Gaps 3;

QY 147 CAGGACTATGTTGAGCTGAAGGCTTCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 206
 DB 338 CAGGACTATGTTGAGCTGAAGGCTTCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 206
 QY 207 GGGGCGGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 266
 DB 398 GGGGCGGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 266
 QY 267 GGTGCGGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 323
 DB 458 GGTGCGGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 323
 QY 324 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 383
 DB 518 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 383
 QY 518 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 383
 DB 384 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 443
 QY 578 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 503
 DB 444 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 503
 QY 638 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 694
 DB 504 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 694
 QY 695 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 754
 DB 755 GTACGCTGAGGCTGAGGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 754
 QY 624 AAAATACGCGGAGCTATGAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 683
 DB 806 AAAATACGCGGAGCTATGAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 683
 QY 684 CCGTGAAGGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 743
 DB 806 CCGTGAAGGAGCAAGGCTTCCAGAGCTATGTTGACTGAAGCTTCAAGCGT 743

Db CCTGTGAAAAGGACCTCTCCCAATGTTGCCGAAATGCCATTGCACTGTAAGCT 925
QY 744 GGTGACCTACGACATCTTCAGAGAGAGAGCTGTGATACCACTGCTCACTGACAACTT 803
Db 926 GGTGACCTACGACATCTTCAGAGAGAGAGCTGTGATACCACTGCTCACTGACAACTT 985
QY 804 CCCCTGACCTTGTCTCTGCTTTGAGACCGGCTTGTGTGACAGAGTGTGCTCCCTCC 863
Db 986 CCGTGTGCACTTCACTTCTGCTTGGGGGCTTGTGACCACTGATGCTCTCCCTCC 1045
QY 864 GGTGACGCTGTGAGAGACCGGATATGAACTCACTTCAGGCACTTCACTGACGCTT 923
Db 1046 CTTGATGTGTGTCAGACAGATATATGAACTTCTGCTTGGGCACTGACAGGCGCT 1105
QY 924 CGACTGATATGATTAAGATGTGGCCCGAGAGAGGCGCCCAAGCTTCTCAAGAGATTTAC 983
Db 1106 CCACTGTGCTGACCATCTCCGAGAGAGAGGCGCCCAAGCTTCTCAAGAGGCTTCACT 1165
QY 984 ACCCTGCTTTTGTGCTTGGGATCTGTGAACGTGTGATGTTCTGTAACCTATGAGAGCT 1043
Db 1166 GCTTCTCTTCTCTCCGCTTGGGATCTGTGAACGTGTGATGTTCTGTAACCTATGAGAGCT 1225
QY 1044 GAAAGGCGGCTGTGATGAAGTCCAGATGTTACGGGAGATGACCGTTTGAACAAGACAGA 1103
Db 1226 CAAAGGCGGCTGTGATGCTGCTATGATTCGGGAGGACCTTTTGAAGCTTCTCAGC 1285
QY 1104 AGGCCACTGTAGC 1117
Db 1286 TGATGACTGTAGC 1299

RESULT 7
US-10-152-319A-1731

Sequence 1731, Application US/10152319A

Publication No. US20040072160A1

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

APPLICANT: Porter, Mark

APPLICANT: Johnson, Kory

APPLICANT: Hise, Brandon

APPLICANT: Castle, Arthur

APPLICANT: Blahoff, Michael

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5089-US

CURRENT APPLICATION NUMBER: US/10152,319A

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: US 60/292,335

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 60/297,523

PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,925

PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,810

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,807

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,808

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/315,047

PRIOR FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: US 60/324,928

PRIOR FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/330,867

PRIOR FILING DATE: 2001-11-01

PRIOR APPLICATION NUMBER: US 60/330,462

PRIOR FILING DATE: 2001-10-22

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2221

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 1731

LENGTH: 1575

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_019354
US-10-152-319A-1731Query Match 39.8%; Score 490; DB 12; Length 1575;
Best Local Similarity 71.3%; Pred. No. 2,6e-133;
Matches 694; Conservative 0; Mismatches 265; Indels 15; Gaps 3;

QY 147 CAGACATATGTTGAGTGAAGCTTCAAGAGTGTCTCCACATGAGCTGTGAATTTCT 206
Db 338 CAGATATATGTTGAGTGAAGCTTCAAGAGTGTCTCCACATGAGCTGTGAATTTCT 397
QY 207 GGGGGCAGGACAGAGAGCTGTGTTGCTGACCTCGTTACCTTCCACTGAGACAGCCAA 266
Db 398 GGGGGCAGGACAGAGAGCTGTGTTGCTGACCTCGTTACCTTCCACTGAGACAGCCAA 457
QY 267 GGTGCGCTGACATATCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
Db 458 AGTCCGCTGACATATCAG 517
QY 324 GTACCGTGTGCTGTGAG 383
Db 518 GTACCGGCGGTGTGAG 577
QY 384 CTACATGAGGCTGTGAG 443
Db 578 CTACATGAGGCTGTGAG 637
QY 444 CCTATGATCTCGTCAAG 503
Db 638 CCTATGATCTCGTCAAG 694
QY 504 TACCGGATTTTGTGAG 563
Db 695 GAGCGGCTCTGTGAG 754
QY 564 AGATGTGTGAG 623
Db 755 AGATGTGTGAG 805
QY 624 AAAATACAGCGGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 683
Db 806 GAGATACAG 865
QY 684 CCTGTGAAAAGAACTTGTCCCAATCATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
Db 866 CCTGTGAAAAGAACTTGTCCCAATCATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 925
QY 744 GGTGACCTACGACATCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
Db 926 GGTGACCTACGACATCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
QY 804 CCCCTGACCTTGTCTCTGCTTTGAGACCGGCTTGTGTGACAGAGTGTGCTCCCTCC 863
Db 986 CCGTGTGCACTTCACTTCTGCTTGGGGGCTTGTGACCACTGATGCTCTCCCTCC 1045
QY 864 GGTGACGCTGTGAGAGACCGGATATGAACTCACTTCAGGCACTTCACTGACGCTT 923
Db 1046 CTTGATGTGTGTCAGACAGATATATGAACTTCTGCTTGGGCACTGACAGGCGCT 1105
QY 924 CGACTGATATGATTAAGATGTGGCCCGAGAGAGGCGCCCAAGCTTCTCAAGAGATTTAC 983
Db 1106 CCACTGTGCTGACCATCTCCGAGAGAGAGGCGCCCAAGCTTCTCAAGAGGCTTCACT 1165
QY 984 ACCCTGCTTTTGTGCTTGGGATCTGTGAACGTGTGATGTTCTGTAACCTATGAGAGCT 1043
Db 1166 GCTTCTCTTCTCTCCGCTTGGGATCTGTGAACGTGTGATGTTCTGTAACCTATGAGAGCT 1225
QY 1044 GAAAGGCGGCTGTGATGAAGTCCAGATGTTACGGGAGATGACCGTTTGAACAAGACAGA 1103
Db 1226 CAAAGGCGGCTGTGATGCTGCTATGATTCGGGAGGACCTTTTGAAGCTTCTCAGC 1285
QY 1104 AGGCCACTGTAGC 1117

Db 836 GCCCTCTTTCGCTGGGTTCTCGAGAGTGTGATGTTCTGACATGAGACACT 895
 QY 1044 GAAAGGCGCCCTGATGAAAGTCAATGTAGGGAATCACCGTTTGAAC 1094
 Db 896 GAAAGAGCCCTCATGCTGCTGCACTTCCGAGAGGCTCCCTTCTAGC 946

RESULT 9

US-09-886A-3
 ; Sequence 3, Application US/09823886A
 ; Publication No. US20030150022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Newell, Martha
 ; APPLICANT: Berry-Lowe, Sandra
 ; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
 ; FILE REFERENCE: C1102/7002
 ; CURRENT APPLICATION NUMBER: US/09/823,886A
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: US 60/193,533
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1105
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-823-886A-3

Query Match 38.7%; Score 476.6; DB 10; Length 1105;
 Best Local Similarity 71.2%; Pred. No. 2e-129;
 Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

QY 147 CAGGACTATGTTGACTGAAGCTTCAAGACGTGCTCCACCATGCTGTGAATTCCT 206
 Db 82 CAGCATCATGTTGGTTGAGGTTCAAGGCCACAGATGTCCTTACGACATGTGAAGTTCT 141
 QY 207 GGGGGGAGGACAGACGAGCCGTTTGTCTGACCTGTTACCTTTCACCTGAGACAGCCAA 266
 Db 142 TGGGGGTTGACAGCTGCTGCTGATCGCAATCTCACTTCTCTGTGATGCTTAA 201
 QY 267 GGTCCGCTGACAGATCCAGGGGAGAACAG--CGGTTCAGACGCGCCGCTGTGCA 323
 Db 202 AGTCGGTTTACAGATCCAGAGAAAGTCAAGGGGCAAGTGCCTGCTACAGCCAGCCCA 261
 QY 324 GTACCGTGGCTGCTGGGCACTCTTACATGATGTCGAGAGTGAAGGTTCCCTGAGCCC 383
 Db 262 GTACCGGCTGTGATGGGCACTTCTGACATGTGCTGACATGAGGGCCGCCGAGGCT 321
 QY 384 CTACATATGCTGCTGGGCGGCGGCTGAGGCGCAGATGAGCTTGCCTCCATCCGATCGG 443
 Db 322 CTACATATGCTGCTGGGCGGCGGCTGAGGCGCAGATGAGCTTGCCTCCATCCG 381
 QY 444 CCTCTATGACTCCGTCAAGAGGTGTACACCCCAAGGCGGAGCACTCCAGCTTCA 503
 Db 382 CCTGTATGATTCGTGAACAGTTTCA--CCAAGGCTGTGAGATCCAGCATTTG 438
 QY 504 TACCGGATTTGGCGGCTGACACACAGAGCCATGGCGGTGACCTGTGCTCCAGCCAC 563
 Db 439 GACCCGCTCTGACAGGCAACACAGGTGCTGCGCTGTGCTGTGCTGAGCCAC 498
 QY 564 AGATGTGTGAAGTTCGATTTTCAAGGCGCAGATACCTGCGGCACTCAGAGCAG 623
 Db 499 GATGTGTGAAGTTCGATTTTCAAGC-----TCAAGCCCGGCTGAGAGTGTG 549
 QY 624 AAATATCAGCGGACTATGACGCTTACAGAACCATCCAGAGAGAGAGTCAAGGG 683
 Db 550 GATATTCAGAGCAGCTCATGCTTACAGAACCATTTGCGAGAGAGGTTCCGCGG 609
 QY 684 CTTGTGAAGAACTTTGCCCAATCAAGAGAAATGCTATGCTCACTGTCTAGGT 743
 Db 610 CCTCTGAAAGGAGCTCTCCCAATGTGTCTGTATGCTCACTGTCTGAGCT 669

QY 744 GATGACTTACGACATCTCTCAAGAGAGAGTCTGAGTACCACTGTCTCACTGACACTT 803
 Db 670 GATGACTTATGACCTCATCAAGATGCTCTCTGAAGCCCAACTCAGACAGATGACCT 729
 QY 804 CCCCTGCACTTTTGTCTGCTTTGAGCGGCTTGTGTCACAGTGTGCTCC 863
 Db 730 CCTTGCACCTTCACTTGTGCTTTGGGAGGCTTGTGACACATCTGATGCTCTCC 789
 QY 864 GGTGACGTGTGAGAGCCCGATATATGACTCACTTCCAGGCGATCTTACGCCCT 923
 Db 790 TGTAGACGTGTCAAGAGATATCATGAACTTCTGCGCCGAGTACAGTACGCTG 849
 QY 924 GACTGTATATTAAGATGTGGCCAGAGGCGCCCAAGCTTCTCAAGGATTTAC 983
 Db 850 CCACTGTCCCTTACATGCTTCCAGAGAGGCGCCGAGGCTTCTCAAGGATTTAT 909
 QY 984 ACCCTCTTTTGGTGGATCCCTGAGAGTGTGATGTTCTGTAACCTATGACACT 1043
 Db 910 GCCCTCTTCTCCGCTTGGGTTCTGGAAGTGTGATGTTCTGACCTATGAGCAGCT 969
 QY 1044 GAAAGGCGCCCTGATGAAAGTCCAGATGTTCAGGAAATCACCGTTTGAAC 1094
 Db 970 GAAAGAGCCCTCATGCTGCTGCTGCACTTCCGAGAGGCTCCCTTCTAGC 1020

RESULT 10

US-10-265-689-13
 ; Sequence 13, Application US/10265689
 ; Publication No. US2003011975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SURMIT, RICHARD S.
 ; APPLICANT: COLBINS, SHEILA A.
 ; APPLICANT: WARDEN, CRAIG H.
 ; APPLICANT: SELDIN, MICHAEL F.
 ; APPLICANT: RICQUIER, DANIEL
 ; APPLICANT: BOUTLAND, FREDERIC
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
 ; FILE REFERENCE: 1579-376
 ; CURRENT APPLICATION NUMBER: US/10/265,689
 ; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/353,645
 ; PRIOR FILING DATE: 1999-07-15
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864
 ; PRIOR FILING DATE: 1997-04-22
 ; PRIOR APPLICATION NUMBER: 60/034,960
 ; PRIOR FILING DATE: 1997-01-15
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1612
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-265-689-13

Query Match 38.7%; Score 476.6; DB 15; Length 1612;
 Best Local Similarity 71.2%; Pred. No. 2.3e-129;
 Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

QY 147 CAGGACTATGTTGACTGAAGCTTCAAGAGGCTCCACCATGCTGTGAATTCCT 206
 Db 338 CAGCATCATGTTGGTTGAGGTTCAAGGCCACAGATGTCCTTACGACATGTGAAGTTCT 397
 QY 207 GGGGGGAGGACAGACGCTGTTTGTGACCTGTTTACCTTTCACCTGAGACAGCCAA 266
 Db 398 TGGGGGTTGACAGCTGCTGATGCAATGTCACTTCTCTGGAATCTCTTAA 457
 QY 267 GGTCCGCTGACAGATCCAGGGGAGAACAG--CGGTTCAGACGCGCCGCTGTGCA 323
 Db 458 AGTCCGTTTACAGATCCAGAGAAAGTCAAGGGGCAAGTGCCTGCTACAGCCAGCCCA 517
 QY 324 GTACCGTGGCTGCTGGGACCATCTTACATGATGTGCTGAGAGTGAAGGTTCCCTGAGCC 383
 Db 518 GTACCGGCTGTGATGGGACCATTTCTTACATGTGTGCTGATGAGGGCCGCCGAGGCT 577

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QY 384 CTACATGAGGCTGTGGCCGGCTTGCAGAGCCAGATGAGCTTGCCTTCATCCGATCGG 443
DB 578 CTACATGAGGCTGTGGCCGGCTTGCAGAGCCAGATGAGCTTGCCTTCATCCGATCGG 637
QY 444 CCTTATGACTCCGTCAGAGAGTGTACACCCCCAAAGGCGGAGACATCCAGCTCAG 503
DB 638 CCTTATGACTCCGTCAGAGAGTGTACACCCCCAAAGGCGTGTAGACATCCAGCTCAG 694
QY 504 TACCGGAAATTTGGCCGGCTGCACCAAGAGCCATGAGGCTGTAGCCCTGAGCCAGCCAC 563
DB 695 GAGCCGCTCTTACAGAGAGAGACCAAGAGTCCCTGCTGTGTGTGCTGTGCTGAGCCAG 754
QY 564 AGATGTGTGAAGTTCGATTCAGGCGCAGATACCTCGGCGCATCCAGAGAGCCAGAG 623
DB 755 GATGTGTGAAGTTCGATTCAGGCGCAGATACCTCGGCGCATCCAGAGAGCCAGAG 805
QY 624 AAAATACAGCGGAGCTATGAGAGCCCTACAGAACATTCGCGAGAGAGAGAGAGTCA 683
DB 806 GAGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 865
QY 684 CCGTGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
DB 866 CCGTGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 925
QY 744 GGTGACCTACGACATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
DB 926 GGTGACCTACGACATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
QY 804 CCGCTGACCTTGTGTCTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
DB 986 CCGCTGACCTTGTGTCTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1045
QY 864 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
DB 1046 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1105
QY 924 CGACTGTATGATTAAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
DB 1106 CGACTGTATGATTAAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1165
QY 984 ACCCTCTTTTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
DB 1166 GGCCTCTTTTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1225
QY 1044 GAAACGAGCCCTGATGAAGTCCAGATGTTCAGGAGATCAACGTTTGAAC 1094
DB 1226 GAAACGAGCCCTGATGAAGTCCAGATGTTCAGGAGATCAACGTTTGAAC 1276

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RESULT 11

US-10-240-965-183

Sequence 183, Application US/10240965

Publication No. US20030165924A1

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: SHIFFMAN, DOV

APPLICANT: SOMOGYI, ROLAND

APPLICANT: LAMN, RICHARD M.

APPLICANT: SEILHAMER, JEFFREY J.

APPLICANT: PORTER, GORDON J.

APPLICANT: MIKITA, THOMAS

APPLICANT: TAI, JULIE

APPLICANT: TAI, JULIE

TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION

FILE REFERENCE: PA-0025 PCT

CURRENT APPLICATION NUMBER: US/10/240, 965

PRIOR FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: 60/195,106

NUMBER OF SEQ ID NOS: 276

SOFTWARE: PERL Program

SEQ ID NO 183

LENGTH: 1643

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 093687.6.
US-10-240-965-183

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Query Match 38.7%; Score 476.6; DB 15; Length 1643;
Best Local Similarity 71.2%; Pred. No. 2,3e-129;
Matches 677; Conservative 0; Mismatches 259; Indels 15; Gaps 3;

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QY 147 CAGGACTATGTTGATGAGAGCTTCAAGAGCTGCTCCACATGAGCTGTGAAGTTCT 206
DB 366 CAGGACTATGTTGATGAGAGCTTCAAGAGCTGCTCCACATGAGCTGTGAAGTTCT 425
QY 207 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 266
DB 426 TGGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
QY 267 GGTGCGCTGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
DB 486 AGTCCGCTTACAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
QY 324 GTACCGTGGCGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
DB 546 GTACCGTGGCGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
QY 384 CTACATGAGGCTGTGGCCGGCTTGCAGAGCCAGATGAGCTTGCCTTCATCCGATCGG 443
DB 606 CTACATGAGGCTGTGGCCGGCTTGCAGAGCCAGATGAGCTTGCCTTCATCCGATCGG 665
QY 444 CCTTATGACTCCGTCAGAGAGTGTACACCCCCAAAGGCGGAGACATCCAGCTCAG 503
DB 666 CCTTATGACTCCGTCAGAGAGTGTACACCCCCAAAGGCGTGTAGACATCCAGCTCAG 722
QY 504 TACCGGAAATTTGGCCGGCTGCACCAAGAGCCATGAGGCTGTAGCCCTGAGCCAGCCAC 563
DB 722 TACCGGAAATTTGGCCGGCTGCACCAAGAGCCATGAGGCTGTAGCCCTGAGCCAGCCAC 782
QY 564 AGATGTGTGAAGTTCGATTCAGGCGCAGATACCTCGGCGCATCCAGAGAGCCAGAG 623
DB 782 AGATGTGTGAAGTTCGATTCAGGCGCAGATACCTCGGCGCATCCAGAGAGCCAGAG 843
QY 624 AAAATACAGCGGAGCTATGAGAGCCCTACAGAACATTCGCGAGAGAGAGAGAGTCA 683
DB 843 AAAATACAGCGGAGCTATGAGAGCCCTACAGAACATTCGCGAGAGAGAGAGAGTCA 903
QY 843 GAGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
DB 1014 GAGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
QY 1014 CCGTGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
DB 894 CCGTGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
QY 744 GGTGACCTACGACATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
DB 954 GGTGACCTACGACATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013
QY 804 CCGCTGACCTTGTGTCTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
DB 1014 CCGCTGACCTTGTGTCTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
QY 864 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
DB 1074 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133
QY 924 CGACTGTATGATTAAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
DB 1134 CGACTGTATGATTAAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1193
QY 984 ACCCTCTTTTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
DB 1194 GGCCTCTTTTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1253
QY 1044 GAAACGAGCCCTGATGAAGTCCAGATGTTCAGGAGATCAACGTTTGAAC 1094

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US-10-197-019-2
 ; Sequence 2, Application US/10197019
 ; Publication No. US20030207284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Gilson, Christopher Raleigh
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Parks, Katie E.
 ; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
 ; FILE REFERENCE: MMH-0042US
 ; CURRENT FILING DATE: 2002-07-16
 ; PRIOR APPLICATION NUMBER: US/10/197,019
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-197-019-2

Query Match 38.6%; Score 475.6; DB 16; Length 930;
 Best Local Similarity 71.4%; Pred. No. 3.8e-129;
 Matches 673; Conservative 0; Mismatches 254; Indels 15; Gaps 3;

QY 154 ATGGTTGACGTAAGACCTTTCAGAGTGGCTCCACCATGGCTGTGAAGTTCCTGGGGCA 213
 DB 1 ATGGTTGAGTTTCAGAGCCACAGATGTGCCCTTACTGCCACTGTAAAGTTTCTTGGGCT 60
 QY 214 GGCACAGCAGCCTGTTTGTCTGACCTCTGTAACCTTTCACCTGACACAGCCAGGTCCGC 273
 DB 61 GGCACAGCTGCTGATGAGCATCTCATCACTTTCCTGTGATATCTGTAAGTCCGG 120
 QY 274 CTGCAGATCCAGGGGGAACCAAG--CGGTCCAGAGGCCCGGCTGTGTAGTACCGT 330
 DB 121 TTACAGATCCAGGAAGATCAGGGGCCAGTGCCTGACAGCCAGGCCAGTACCGC 180
 QY 331 GGCCTGCTGGGACCATCTCTGACATGGTGGGAGTCCCTGACGCCCTTACAT 390
 DB 181 GGTGTGATGGGACCATCTCTGACATGGTGGGAGTCCCTGACGCCCTTACAT 240
 QY 391 GGGCTGTGTGCGCGCTGACAGCCAGATGAGCTTGCCTTCATCCGATCGGCTCTAT 450
 DB 241 GGGCTGTGTGCGCGCTGACAGCCAGATGAGCTTGCCTTCATCCGATCGGCTCTAT 300
 QY 451 GACTCGTCAAGCAGGTGTACACCCCAAGGCGGAGACACTCCAGCTCACTACCGG 510
 DB 301 GATTCGTCAACAGATTCTACA---CCAAAGGCTCTGAGCATGCCAGATTGGAGCCGC 357
 QY 511 ATTTGGCGCGGTGACACAGAGCCATGGCGGTGACCTGTGCCAGGCCACAGATGTG 570
 DB 358 CTCTTAGCAGGAGACACAGAGTCCCTGTGGCTGTGGCCAGGCCACAGATGTG 417
 QY 571 GTGAAGTCCGATTTCAAGGCGCAGATACCTCGGGCCATTCAGAGCCAGCAAAATAC 630
 DB 418 GTAAAGTCCGATTTCAAGC-----TCAAGCCCGGCTGAGAGTGTGCGAGATAC 468
 QY 631 AGCGGACTATGAGAGCTTACAGAAACATTCGCAAGGAGAGAGTCAAGGGCCCTGTGG 690
 DB 469 CAAGCACCCTGATGCTTACAGAGCATTGCCCCGAGAGAGGTTCCGGGGCCCTGTGG 528
 QY 691 AAAGGAATTTGCCCAACATCATAGGAATGCTATGCTCACTGTGCTGAGGTGTGACC 750
 DB 529 AAAGGACCTTCTCCCAATTTGTGCTGTATGCTATGTCACTGTGCTGAGCTGTGACC 588
 QY 751 TACGACATCTCAAGAGAGAGCTGTGACTACACACTGTCTCATCTGACAACCTTCCCTGC 810
 DB 589 TATGACCTCATAGAGATGCCCTCTGAAAGCCACCTCATGACAGATGACCTCCCTTGC 648
 QY 811 CACTTGTCTGTGCTTGTGAGCGGCTTCTGTGCCACAGTGTGGCTTCCCGGTGAGAC 870

DB 649 CACTTCATTTCTGCTTGTGGGGCAGGCTTCTGACACACTGTCATGCGCTCCCTGTAGAC 708
 QY 871 GTGTGAAGACCCGCTATATGAACTCACTTCAGGCCAGATCTTCAAGCCCTGACTGT 930
 DB 709 GTGTCAAGACGATATCATGAACTTGCCCTGTGGCCAGTACAGTAGCGCTGCGCATGT 768
 QY 931 ATGATTAAGATGTGGGCCAGAGAGGCCCAAGCCTTCTTCAAGAGGATTTAACAACCTCC 990
 DB 769 GCCCTTACAGCTCCAGAAAGAGGGGCCAGAGCCTTCTTCAAAAGGTTCAATGCTCC 828
 QY 991 TTTTGGTTTGGATCCTGGAACGTGTGATGTTCTGTAACCTTATAGACAGCTGAAACGG 1050
 DB 829 TTCTTCGCTTGGGTTCTCTGAAAGTGTGATGTTCTGACCTTATAGACAGCTGAAACGA 888
 QY 1051 GCCCTGATTAAGTCCAGATGTTACGGGAATCACCGTTTGA 1092
 DB 889 GCCCTAGGCTGCTGCACTTCCGAGAGGCTCCCTTCTGA 930

Search completed: May 18, 2004, 16:16:22
 Job time : 594 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 11:18:36 ; Search time 3063 Seconds
(without alignments)
12001.418 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estbm:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
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29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|------------|-------|-------------|--------|-------|--------------------|
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| 2 | 680.6 | 55.3 | 927 | 29 | AY406946 Mus muscu |
| 3 | 611.2 | 49.7 | 808 | 13 | BU745943 CH2#003 H |
| 4 | 595.6 | 48.4 | 602 | 29 | AY406945 Pan trogl |

| 5 | 519.2 | 42.2 | 613 | 9 | AL596731 |
|----|-------|------|------|----|----------|
| 6 | 489.4 | 39.8 | 364 | 11 | AK054060 |
| 7 | 487.8 | 39.6 | 364 | 11 | AK035298 |
| 8 | 486.8 | 39.5 | 930 | 29 | AY413339 |
| 9 | 474 | 38.5 | 930 | 29 | AY413337 |
| 10 | 448.2 | 36.4 | 1101 | 14 | CK024683 |
| 11 | 434.2 | 35.3 | 673 | 12 | BM986146 |
| 12 | 432.8 | 35.2 | 612 | 10 | BF670349 |
| 13 | 423.8 | 34.4 | 1181 | 14 | CK025514 |
| 14 | 420.8 | 34.2 | 930 | 29 | AY413338 |
| 15 | 405.4 | 32.9 | 927 | 12 | BI248501 |
| 16 | 394.2 | 32.0 | 938 | 12 | BI692548 |
| 17 | 388.2 | 31.5 | 404 | 9 | AA192136 |
| 18 | 385 | 31.3 | 892 | 12 | BI904624 |
| 19 | 381.6 | 31.0 | 876 | 14 | CF374967 |
| 20 | 381.2 | 31.0 | 891 | 14 | CA474512 |
| 21 | 380.8 | 30.9 | 807 | 12 | BG757774 |
| 22 | 377.6 | 30.7 | 766 | 12 | BG976754 |
| 23 | 374.6 | 30.4 | 794 | 12 | BG968126 |
| 24 | 373.6 | 30.3 | 684 | 14 | CB446089 |
| 25 | 369.8 | 30.0 | 739 | 14 | CA944705 |
| 26 | 368.4 | 29.9 | 825 | 14 | CF147551 |
| 27 | 364.6 | 29.6 | 913 | 14 | CA787496 |
| 28 | 362.4 | 29.4 | 573 | 12 | BM986209 |
| 29 | 360.2 | 29.3 | 1159 | 10 | CD501350 |
| 30 | 356.8 | 29.0 | 782 | 10 | BF974251 |
| 31 | 355.4 | 28.9 | 739 | 14 | CF766488 |
| 32 | 354.6 | 28.8 | 697 | 12 | BG965001 |
| 33 | 353.2 | 28.7 | 701 | 9 | AI430170 |
| 34 | 352 | 28.6 | 909 | 14 | CF265879 |
| 35 | 351 | 28.5 | 912 | 14 | CF266280 |
| 36 | 350.8 | 28.5 | 888 | 14 | CA474222 |
| 37 | 350.4 | 28.5 | 818 | 12 | BI904048 |
| 38 | 349.6 | 28.4 | 813 | 14 | CK017263 |
| 39 | 347 | 28.2 | 850 | 14 | CA475173 |
| 40 | 345.4 | 28.1 | 739 | 14 | CA379425 |
| 41 | 344.2 | 28.0 | 890 | 13 | BO960193 |
| 42 | 344 | 27.9 | 832 | 14 | CF150802 |
| 43 | 342.8 | 27.8 | 742 | 14 | CK126808 |
| 44 | 342.6 | 27.8 | 764 | 14 | CK017963 |
| 45 | 340.4 | 27.7 | 932 | 12 | BI258707 |

ALIGNMENTS

RESULT 1
LOCUS AY406944
DEFINITION Homo sapiens UCP3 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY406944
VERSION AY406944.1 GI:39762915
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 939)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 939)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT

FEATURES

SOURCE

1. 939
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>939
/gene="UCP3"
/locus_tag="HCM2726"

gene

ORIGIN

Query Match 76.3%; Score 939; DB 29; Length 939;
Best Local Similarity 100.0%; Pred. No. 7.5e-200; Indels 0; Gaps 0;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ATGGTTGAGCTGAAGCCTTTCAGACGTCCTCCACCATGCTGTGAAGTTCTGAGGCGCA 60
214 GGCAACAGACGCTGTTTGTCTGACCTCTGTTACCTTTCCATGAGACACAGCCCAAGTCCGC 273
61 GGCAACAGACGCTGTTTGTCTGACCTCTGTTACCTTTCCATGAGACACAGCCCAAGTCCGC 120
274 CTGCAGATCCAGAGGAGAGAACACAGCGGCTCCAGACGCGCCGCTGTCAGATACCGTGGC 333
121 CTGCAGATCCAGAGGAGAGAACACAGCGGCTCCAGACGCGCCGCTGTCAGATACCGTGGC 180
334 GTGCTGGGACCATCTCTGACATGCTGTCAGATGAGGCTCCCTGACGCCCTTACATATGG 393
181 GTGCTGGGACCATCTCTGACATGCTGTCAGATGAGGCTCCCTGACGCCCTTACATATGG 240
394 CTGCTGGGACCATCTCTGACATGCTGTCAGATGAGGCTCCCTGACGCCCTTACATATGG 453
241 CTGCTGGGACCATCTCTGACATGCTGTCAGATGAGGCTCCCTGACGCCCTTACATATGG 300
454 TCCGTCAGACAGTGTACACCCCAAGGCGGAGCACTCCAGCCTCACTACCGGAGT 513
301 TCCGTCAGACAGTGTACACCCCAAGGCGGAGCACTCCAGCCTCACTACCGGAGT 360
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361 TTGGCCGGCTGACCAACAGAGCCATGCGGTGACCTGTGCCCAGCCCAAGATGTGTG 420
574 AAGGTCGCAATTCAGAGCCCAACATCCTCGGCGCATTCAGAGGAGCAAGAAATACAGC 633
421 AAGGTCGCAATTCAGAGCCCAACATCCTCGGCGCATTCAGAGGAGCAAGAAATACAGC 480
634 GGACATCTCAAGAGAGAGCTGCTGACATACCTCTGCTCACTGACCACTTCCCTGCGAC 693
481 GGACATCTCAAGAGAGAGCTGCTGACATACCTCTGCTCACTGACCACTTCCCTGCGAC 540
694 GGAATCTTCCCAACATCATGAGAGATGCTATGTCACCTGTGCTGAGGTGTGACTTAC 753
541 GGAATCTTCCCAACATCATGAGAGATGCTATGTCACCTGTGCTGAGGTGTGACTTAC 600
754 GACATCTCAAGAGAGAGCTGCTGACATACCTCTGCTCACTGACCACTTCCCTGCGAC 813
601 GACATCTCAAGAGAGAGCTGCTGACATACCTCTGCTCACTGACCACTTCCCTGCGAC 660
814 TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
661 TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
874 GTGAAGACCCGCTATATGAATCACTCAAGGCAAGTCACTTCAAGCCCTGCACTGTATG 933
721 GTGAAGACCCGCTATATGAATCACTCAAGGCAAGTCACTTCAAGCCCTGCACTGTATG 780
934 ATTAAGATGTGGCCCAAGAGAGGCGCCCAAGCCTTCAAGAGGATTTTCAACCTCTCTT 993
781 ATTAAGATGTGGCCCAAGAGAGGCGCCCAAGCCTTCAAGAGGATTTTCAACCTCTCTT 840

QY 994 TTGGCTTTGGATCCTGGAACGTGTGTATGTTCTGTAACCTATGAGCAGCTGAACCGGCC 1053
DB 841 TTGGCTTTGGATCCTGGAACGTGTGTATGTTCTGTAACCTATGAGCAGCTGAACCGGCC 900
QY 1054 CTGATGAAGATCCAGATGTTACGGGAATCACCCTTTTGA 1092
DB 901 CTGATGAAGATCCAGATGTTACGGGAATCACCCTTTTGA 939

RESULT 2

AY406946

LOCUS

DEFINITION

MUS MUSCULUS UCP3 GENE, VIRTUAL TRANSCRIPT, PARTIAL SEQUENCE.

ACCESSION

AY406946

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

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JOURNAL

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Db 222 CTGTCGCTGCGCTGACCGCCAGATGATTTGCTCCATTGCAATTGGCTCTTACGAC 291
 Qy 454 TCCGTCAAGCAGGTGTACACCCCAAGCGCGGAACTTCCAGCTCTCACTACCGGATT 513
 Db 222 TCTGTCAAGCAGGTGTACACCCCAAGCGCGGAACTTCCAGCTCTCACTACCGGATT 351
 Qy 514 TTGGCCGCGTGCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 573
 Db 352 CTGGAGGCGTGCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 411
 Qy 574 AAGTCCGATTTTCAGGCGCAGCTACCTCGGCGCTCCAGAGGAGGAGGAGGAGGAGGAGGAG 633
 Db 412 AAGTCCGATTTTCAGGCGCAGCTACCTCGGCGCTCCAGAGGAGGAGGAGGAGGAGGAGGAG 468
 Qy 634 GGGAGTATGAGAGCGCTTACAGAAACCATCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 693
 Db 469 GGGAGTATGAGAGCGCTTACAGAAACCATCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 528
 Qy 694 GGAATCTTGGCCCAATCATCTGAGAGAAATGCTATCGTCACTGAGGAGGAGGAGGAGGAGGAG 753
 Db 529 GGGAGTATGAGAGCGCTTACAGAAACCATCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 588
 Qy 754 GACATCTTCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813
 Db 589 GACATCTTCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 648
 Qy 814 TTGTCTCTGCTTGGAGCGCGCTTCTGTGCGACAGTGTGCGCTCCCGGTGAGCGTG 873
 Db 649 TTGTCTCTGCTTGGAGCGCGCTTCTGTGCGACAGTGTGCGCTCCCGGTGAGCGTG 708
 Qy 874 GTGAGAGCCCGGTATATGAACTCACTCCAGGCGGAGTACTTCAAGGCGGCTTCACTGTATG 933
 Db 709 GTGAGAGCCCGGTATATGAACTCACTCCAGGCGGAGTACTTCAAGGCGGCTTCACTGTATG 768
 Qy 934 ATTAAGATGTGGCCAGAGAGGCGCCACAGCTTCTCAAGAGGAGTTCACCTCTCTT 993
 Db 769 CTGAAGATGTGGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
 Qy 994 TTGCGTTGGGATCTCTGAAAGCTGTGATGTTCTGTAACCTATGAGGAGGAGGAGGAGGAGGAG 1053
 Db 829 CTGCGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 888
 Qy 1054 CTGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1092
 Db 889 TTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 927
 RESULT 3
 BUI45943 808 bp mRNA linear EST 10-OCT-2002
 LOCUS CH2#003_H04T7 Canine heart normalized cDNA library in pBluescript
 DEFINITION Canis familiaris cDNA clone CH2#003_H04 5', mRNA sequence.
 ACCESSION BUI45943
 VERSION BUI45943.1 GI:23695606
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Mammalia; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 808)
 Y1.Y., Desai, R., Olatte, M., Henthorn, P. and George A.L.
 Expressed sequence tags from Canine heart
 Unpublished (2003)
 Contact: George AL
 Division of Genetic Medicine
 Vanderbilt University
 529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
 Tel: 615 936 2660
 Fax: 615 936 2661
 Email: al.george@vanderbilt.edu
 Insert Length: 1782 Std Error: 0.00
 Seq primer: T7: TAAATGACTCACTATAGGG
 High quality sequence start: 40

FEATURES High quality sequence stop: 637.
 source Location/Qualifiers
 1..808
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /clone="CH2#003_H04"
 /tissue_type="heart"
 /cell_type="heart"
 /dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"
 /clone_lib="Canine heart normalized cDNA library in pBluescript"
 /note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"
 ORIGIN
 Query Match 49.7%; Score 611.2; DB 13; Length 808;
 Best Local Similarity 87.6%; Pred. No. 2.5e-126;
 Matches 691; Conservative 0; Mismatches 94; Indels 4; Gaps 2;
 Qy 309 GGGCCGGCTGTCAGTACCGTGTGCGGACCAATCTGACCATGATGTCGACTGA 368
 Db 22 GGGCGGTCCGGCTGAGCGCGGTGTGCTG3CACCACTGACCATGATGTCGACCA 81
 Qy 369 GGGTCCCTGACCGCTCAATAGGCTGGTGGCCGCTGACAGCGCAGATGAGTTCGC 428
 Db 82 GGGCGCGCG-AAGCCTTACACGGGTGTCCCGGCTGACAGCGCAGATGAGTTCGC 140
 Qy 429 CTCATCCGATCGGCTCTATGACTCGTCAAGAGGTGTACACCCCAAGGCGGGA 488
 Db 141 CTCATCCGATGCGCTTATGACTCTGTCAAGAGGTGTACACCCCAAGGAGTCA 200
 Qy 489 CAATTCAGCTCACTACCCGATTTTGGCCGCTGACACCAAGAGGAGGAGGAGGAGGAGGAGGAG 548
 Db 201 CAATTCAGCTCACTACCCGATTTTGGCCGCTGACACCAAGAGGAGGAGGAGGAGGAGGAGGAG 260
 Qy 549 CTGTGCCAGCCCAAGATGTGTGAGAGGTTCGATTTTCAAGGCGAGTACCTCCGCGC 608
 Db 261 ATGTGCCAGCCCAAGATGTGTGAGAGGTTCGATTTTCAAGGCGAGTACCTCCGCGC 318
 Qy 609 ATTCAGAGCGCAGAGAAATACAGCGGAGCTATGACGCTTACAGAACATGCGCAGGGA 668
 Db 319 -GGGGAGACCAAGAGATACAGTGGAGCAATGATGCTTACAGGACATGCGCAGGGA 377
 Qy 669 GGAAGAGTCAAGGCGCTGTGAAAGAACTTGGCCCAATCATGATGAGTGTATCGT 728
 Db 378 AGAAGGGGTCAAGGGGCTATGAAAGAACTTGGCCCAATCATGATGAGTGTATCGT 437
 Qy 729 CAATGTGTGAGAGTGTACCTACGACATCTTCAAGAGAGGAGTGTGATACCACT 788
 Db 438 CAATGTGTGAGAGTGTACCTACGACATCTTCAAGAGAGGAGTGTGATACCT 497
 Qy 789 GCTCACTGACAACTTCCCTGCCATTGTCTGTGCTTTGAGCGCGCTTCTGTGAC 848
 Db 498 GCTCACTGACAACTTCCCTGCCATTGTCTGTGCTTTGAGCGCGCTTCTGTGAC 557
 Qy 849 AGTGTGGCTCCCGCGTGTGAGAGCGGAGTGTGAGAGCGGAGTGTGAGAGCGGAG 908
 Db 558 AGTGTGGCTCCCGCGTGTGAGAGCGGAGTGTGAGAGCGGAGTGTGAGAGCGGAG 617
 Qy 909 GTACTTCAAGCCCTGACCTGTATGATTAAGATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 968
 Db 618 ATACTGAGAG 677
 Qy 969 CTACAGAGGAGTTCACCTCTCTTTTGTGCTTGTGAGATCTGTGAGAGTGTGATGTTGCT 1028
 Db 678 CTATAGGAGTTCACCACTCTTTTGTGCTTGTGAGATCTGTGAGAGTGTGATGTTGCT 737

QY 1029 AACCTATGAGCAGTGAAGCGGCGCTGTGTAAGTCCAGATGTTACGGGAATCACCGTT 1088
 DB 738 GACCTATGAGCAGTGAAGCGGCGCTGTGTAAGTCCAGATGTTACGGGAATCACCGTT 797
 QY 1089 TTGAACAAG 1097
 DB 798 CTGAGTAG 806

RESULT 4
 AY406945 602 bp DNA linear GSS 15-DEC-2003
 LOCUS Pan troglodytes UCP3 gene, VIRUTAL TRANSCRIPT, partial sequence.
 ACCESSION AY406945
 VERSION AY406945.1 GI:39762916
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE 1 (bases 1 to 602)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Periera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 1..602
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..>602
 /gene="UCP3"
 /locus_tag="HCM2726"

ORIGIN
 Query Match 48.4%; Score 595.6; DB 29; Length 602;
 Best Local Similarity 99.3%; Pred. No. 7e-123; Indels 0; Gaps 0;
 Matches 598; Conservative 0; Mismatches 4;

QY 491 ACTCCAGCCTACTACCGGATTTTGGCGGCTGACACAGAGCGATGCGTACCT 550
 DB 1 ACTCCAGCCTACTACCGGATTTTGGCGGCTGACACAGAGCGGATGCGTACCT 60

QY 551 GTGCCAGCCACAGATGTGTGTAAGTCCGATTTTCAGGCCACATACCTCGGCGCAT 610
 DB 61 GTGCCAGCCACAGATGTGTGTAAGTCCGATTTTCAGGCCACATACCTCGGCGCAT 120

QY 611 CCAGAGCCGACAGAAATATCAGCGGAGCTATGACCGCTTACAGAACATATGCGAGGAGG 670
 DB 121 CCAGAGCCGACAGAAATATCAGCGGAGCTATGACCGCTTACAGAACATATGCGAGGAGG 180

QY 671 AAGAGTCAAGGCGCTGTGTAAGAACTTGGCCACATCATGAGGAATGCTATGCTCA 730
 DB 181 AAGAGTCAAGGCGCTGTGTAAGAACTTGGCCACATCATGAGGAATGCTATGCTCA 240

QY 731 ACTGTGTGAGTGTGTGATCAGACATCTTCAAGAGAAAGTGTGACTACCACTGC 790
 DB 241 ACTGTGTGAGTGTGTGATCAGACATCTTCAAGAGAAAGTGTGACTACCACTGC 300

QY 791 TCACGACACTTCCCTCCGACACTTGTCTGTGCTTGGAGCCGCTTCTGTGCAAG 850
 DB 301 TCACGACACTTCCCTCCGACACTTGTCTGTGCTTGGAGCCGCTTCTGTGCAAG 360

QY 851 TGTGGCTCCCTCCGCTGAGCGTGTGTAAGACCCGGTATATGAATCTACCTCCAGCCAGT 910
 DB 361 TGTGGCTCCCTCCGCTGAGCGTGTGTAAGACCCGGTATATGAATCTACCTCCAGCCAGT 420

QY 911 ACTTACGCCCCCTGACCTGTATGATTAAGATGTGTGCGCCAGAGAGGCCCAAGCTTCT 970
 DB 421 ACTTACGCCCCCTGACCTGTATGATTAAGATGTGTGCGCCAGAGAGGCCCAAGCTTCT 480

QY 971 ACAAGGATTTACACCTCTCTTTTGGCTTGGATTCCTGGAACGTGTGATGTTGTTA 1030
 DB 481 ACAAGGATTTACACCTCTCTTTTGGCTTGGATTCCTGGAACGTGTGATGTTGTTA 540

QY 1031 CCTATGACAGCTGTAAGAGCGGCGCTGATGAAGTCCAGATGTTACGGGAATCACCGTTT 1090
 DB 541 CCTATGACAGCTGTAAGAGCGGCGCTGATGAAGTCCAGATGTTACGGGAATCACCGTTT 600

QY 1091 GA 1092
 DB 601 GA 602

RESULT 5
 AL596731 613 bp mRNA linear EST 04-SEP-2003
 LOCUS DKFP451B221.r1.451 (synonym: hlccl) spinal cord Homo sapiens cDNA
 DEFINITION clone DKFP451B221.5', mRNA sequence.
 ACCESSION AL596731
 VERSION AL596731.1 GI:15154427
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 613)
 Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).
 EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).
 Unpublished (1999)
 JOURNAL
 COMMENT
 CONTACT: MIPS
 MIPS
 Ingolstraedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@kitz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No si sequence available.
 This clone (DKFP451B221) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 FEATURES
 source
 1..613
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFP451B221"
 /rname_type="human spinal cord"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_11b="451 (synonym: hlccl) spinal cord"
 /notes="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN
 Query Match 42.2%; Score 519.2; DB 9; Length 613;
 Best Local Similarity 99.3%; Pred. No. 9.9e-106; Indels 1; Gaps 1;
 Matches 532; Conservative 0; Mismatches 3;

QY 1 TCCTGGATGAGCCCTTGAAGAGCCCTGTGTGCTGCTCCCTGCGGCAAGACTCAAGCC 60
 DB 78 TCCTGGATGAGCCCTTGAAGAGCCCTGTGTGCTGCTCCCTGCGGCAAGACTCAAGCC 137
 QY 61 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCCCTGAGCCCTCTCGG 120
 DB 138 CCACCGCTGCACTGAAGCCCAAGGCTGTGAGCAAGCTCTCTCTCCCTGAGCCCTCTCGG 197
 QY 121 CCTTAAAGGAGCTGGGCAAGCCCTTCCAGACTATGTTGAGCTGAAGCCCTTCAAGCGTG 180
 DB 198 CCTTAAAGGAGCTGGGCAAGCCCTTCCAGACTATGTTGAGCTGAAGCCCTTCAAGCGTG 257
 QY 181 CCTCCACCATGCTGTGAGAGTTCTTGGGGGCAAGCAAGCAAGCTGTTTCTGACTCTC 240
 DB 258 CCTCCACCATGCTGTGAGAGTTCTTGGGGGCAAGCAAGCAAGCTGTTTCTGACTCTC 317
 QY 241 GTTACCTTTCACCTGCAACAGCCCAAGGTCCTCCCTGAGATCCAGGGGGAACAAGCGG 300
 DB 318 GTTACCTTTCACCTGCAACAGCCCAAGGTCCTCCCTGAGATCCAGGGGGAACAAGCGG 377
 QY 301 GTCCAGAGGCGCCGCTGCTGAGTACCGTGGCGTGGGCAACCTCTGACCATGTTG 360
 DB 378 GTCCAGAGGCGCCGCTGCTGAGTACCGTGGCGTGGGCAACCTCTGACCATGTTG 437
 QY 361 CGGACTGAGGCTCCTGCAAGCCCTTACCAATGAGGCTGTGCGCGCTGCAAGCGGCAATG 420
 DB 438 CGGACTGAGGCTCCTGCAAGCCCTTACCAATGAGGCTGTGCGCGCTGCAAGCGGCAATG 497
 QY 421 AGCTTGCGCTCCATCGCATCGGCTCTTATGAC-TCCTGCAAGCAAGTGTACACCCCA 479
 DB 498 AGCTTGCGCTCCATCGCATCGGCTCTTATGAC-TCCTGCAAGCAAGTGTACACCCCA 557
 QY 480 AGGCGGGGCAACCTCGAGCTCACTACCGGATTTTGGCGGGTGGCAACCAAGAG 535
 DB 558 AGGCGGGGCAACCTCGAGCTCACTACCGGATTTTGGCGGGTGGCAACCAAGAG 613

RESULT 6
 AK054060 3641 bp mRNA linear HTC 20-SEP-2003
 LOCUS Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
 DEFINITION full-length enriched library, clone:E230015118 product:uncoupling
 protein 2, mitochondrial, full insert sequence.
 ACCESSION AK054060
 VERSION AK054060.1 GI:26343968
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsuno, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format

JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 20530913
 REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 JOURNAL of 60,770 full-length cDNAs
 MEDLINE Nature 420, 563-573 (2002)
 PUBMED 6 (bases 1 to 3641)
 REFERENCE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
 Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
 URL: http://genome-gsc.riken.go.jp, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT CDS
 CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome-gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 URL: http://fantom.qualifiters
 LOCATION/Qualifiers
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ORIGIN
 Query Match 39.8%; Score 489.4; DB 11; Length 3641;

Best Local Similarity 72.0%; Pred. No. 1,1e-98;
Matches 685; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

147 CAGACTATGTTGACTGAGACCTTTCAGACCTGCTCCACCATGCTGTGAATTTCT 206
Db CAGATCATGTTGTTTCAAGGCCAGATGTGCCCCAACAGCACCTGTGAATTTCT 421
Qy GGGGGCAGCAGACGACCTGTTTTCGACCTGTTACCTTTCCACTGAGACAGCCAA 266
Db GGGGGCTGGAGACAGTGTCTGATGACATCTCACTCTTCTCTGGAATACGCCAA 481
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Db GAAACGGGCTGATGAAAGTCCAGATGTTAAGGAGATCAGCGTTTGAAC 1300

RESULT 7
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LOCUS AK035298
DEFINITION Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:95300110 product:uncoupling protein 2,

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AK035298
AK035298.1 GI:26330581
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
11042159

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitasuna, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, B., Katohi, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 403, 685-690 (2001)
11076861

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3964)

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozawa, T.,
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akita, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/

FEATURES
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ORIGIN

Query Match 39.6%; Score 487.8; DB 11; Length 3964;
Best Local Similarity 71.9%; Pred. No. 2.6e-98;
Matches 684; Conservative 0; Mismatches 252; Indels 15; Gaps 3;
147 CAGACATATGTTGAGCTGAACCTTTCAGACGCTCTCCACCATGCTGGAATTCT 206
356 CAGATCATGTTGTTTCAAGGCCACAGATGTGCCCAACAGCCACTGTGAACTTCCA 415
207 GGGGCGACGACACAGAGCTGTTTGTGCACTCGTTACCTTCCACTGGACACAGCCA 266
416 GGGGCTGAGAGAGCTGCTGATTCAGATTCATCTTCCCTGGAATACGCCCA 475
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QY 744 GGTGACCTACAGACATCTTCAAGAGAGAGCTGTGACTACCACTGCTACTGACAACTT 803
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RESULT 8
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LOCUS AY413339

DEFINITION Mus musculus UCP2 gene, VIRIDAL TRANSCRIPT, partial sequence.
ACCESSION AY413339
VERSION AY413339.1 GI:39769301
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 930)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE Science 302 (5652), 1960-1963 (2003)
JOURNAL 14671302
PUBMED 2 (bases 1 to 930)
REFERENCE Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

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Query Match 39.5%; Score 486.8; DB 29; Length 930;
Best Local Similarity 72.2%; Pred. No. 2.2e-98;
Matches 680; Conservative 0; Mismatches 247; Indels 15; Gaps 3;
154 ATGTTGACATGAGCTTCAAGAGCTGCTCCACACAGGCTGTGAGATTTCTGGGGGCA 213

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RESULT 9
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 DEFINITION
 AY413337 930 bp DNA linear GSS 17-DEC-2003
 ACCESSION
 AY413337
 VERSION
 AY413337.1 GI:39769299
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriterra, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D., and Cargill, M.
 TITLE
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL
 Science 302 (5652), 1960-1963 (2003)
 PUBMED
 14671302
 REFERENCE
 AUTHORS
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriterra, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D., and Cargill, M.
 TITLE
 Direct Submissions
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 ORIGIN
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 Best Local Similarity 71.3%; Pred. No. 1.7e-95;
 Matches 672; Conservative 0; Mismatches 255; Indels 15; Gaps 3;
 Qy 154 ATGGTTGAGTGAAGCTTCAAGAGCTGCTCCACATGCTGTGAAGTCTCTGGGGCA 213
 Db 1 ATGGTTGAGTGAAGGCCACAGATGTGCCCTTACTGCTGATGAAGTCTTCTGGGCT 60
 Qy 214 GGCACAGAGCTGTTTGGTGAAGCTGTTACCTTTCATCTGAGACACAGCCAGGTCGGC 273
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 VERSION CK024683.1 GI:38550607
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 ORGANISM Danio rerio
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 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 1101)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabds@mail.nih.gov
 Tissue Procurement: Len Zou, Harvard
 cDNA Library Preparation: Open Biosystems
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
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 /clone="IMAGE:7050599"
 /issue_type="whole body"
 /lab_host="DH10B"
 /clone_idb="NIH_ZGC_10"
 /note="Vector: pEXpress1, Site_1: NotI, Site_2: EcoRV,
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pEXpress-1.
 Library was size-selected for >1 kb fragments. A

ORIGIN

normalized version of this library is also available
 (NIH_ZGC_7). Library was constructed by Open Biosystems
 (Huntsville, AL).
 Query Match 36.4%; Score 448.2; DB 14; Length 1101;
 Best Local Similarity 69.4%; Pred. No. 1.1e-89;
 Matches 641; Conservative 0; Mismatches 273; Indels 9; Gaps 2;

Qy 137 CAGAGCCTTCCAGAGATGTTGGTGAAGAGCTTCAAGAGTGTCTCCACATAGCTG 196
 Db 50 CACAGATTACTGCCGATATGTTGGTCTGAAAGCCCTCAGATGTTCTCTCTGACTG 109
 Qy 197 TGAAGTCTCTGGGGGAGAGGACAGAGGCTGTTTGTGACCTGTTACTTTCACTG 256
 Db 110 TGAAGTGTGAATGACAGAAAGGCGCTGATGCTGATGCTGATGCTGATGCTG 169
 Qy 257 ACACAGCAAGGTCCGCTGACATCAAGGGGAGAAACAGGCGGTCCAGAGCGCCG 316
 Db 170 ACAAGGCCAAGTCCGCTGACAGATCCAGGGGAGAAAGCGGTGACAGAGCGCT 229
 Qy 317 TCGTCAAGTACCGTGGCTGCTGGACCAATCTTCAAGATGTGTGAGTGTGAGT 376
 Db 230 GCATCCGCTACAAAGGTGTTTCCGAGACATCAAGCATATGAGAGCGAGGTCCG 289
 Qy 377 GCAAGCCCTTACAAATGGCTGTGTGGCGGCTGCAAGGCGGAGATGAGTTCGCT 436
 Db 290 GCTGCTTACAAAGGCTGTGTGGCGGCTGCAAGGCGGAGATGAGTTCGCTCAT 349
 Qy 437 GCATGGGCTCTATATGCTCCGTCAGAGAGTGTATCAACCCCAAGGCGGAGCA 496
 Db 350 GATTTGGCTCTTACAGACAAAGTCAAGAGCTTCTACAGC---GTGAAAGAACCC 406
 Qy 497 GCTTCAATCCGAGATTTTGGCGGCTGACCAAGAGGAGGAGGAGGAGGAGGAG 556
 Db 407 ATGTGGCGGTGGAATCTGCGGCGCTGTATCAACGAGAGGAGGAGGAGGAGG 466
 Qy 557 AGCCCAAGATGTGTGAAGTGTGAGTTCAGGCTTCAAGATCACTTGGGCTATC 616
 Db 467 AGCCCAAGATGTGTGAAGTGTGAGTTCAGGCTTCAAGATCACTTGGGCTATC 520
 Qy 617 GCGAAGAAATATACGCGGAGCTATGAGCGCTTACAGAAACATCCGCGAGAG 676
 Db 521 TGGGAGAGATATCAACGAGCAATGACGCTTACAGGAGATCTTCAAGTGAAG 580
 Qy 677 TCAGGGGCTGTGAAAGAACTTGGCCATCATGAGAGATCTATGCTCAACTGT 736
 Db 581 TCGTGTCTCTGAAAGAACTTGGCCATCATGAGAGATCTATGCTCAACTGT 640
 Qy 737 CTGAGTGTGATCTACGATCTCTCAAGAGAGAGTGTGATCTACCTGCTCAGT 796
 Db 641 CAGAACTGTGTCTTACGATCTGATCAAGAGGCTATCTTAAACAGAGCTGTG 700
 Qy 797 ACAACTTCCCTGACACTTGTGCTGCTTGTGAGCGGCTTGTGACAGAGTGTG 856
 Db 701 ACAACTTCCCTGACACTTGTGCTGCTTGTGAGCGGCTTGTGACAGAGTGTG 760
 Qy 857 CCTCCCGGTGAGCGTGTGAAAGACCCGGTATATGAATCTACCTCCAGGCTG 916
 Db 761 CGTCTCTGTGATGTGTGAAAGACCGGTATATGAATCTACCTCCAGGCTG 820
 Qy 917 GCGCCCTGACATGTATGATTAAGATGTGAGCCCAAGAGGCGCCCAAGCTTCA 976
 Db 821 GGTCCACAACTGCGCTGAGCAATGCTCAAGAGGAGGAGGAGGAGGAGGAGG 880
 Qy 977 GATTTAACAACCTCTTTTGTGCTTGTGAGTCTTGTGAGTGTGATGTTCTGTA 1036
 Db 881 GTTTTGTCTCTGATCTCTGCGCGCTGAGTCTGAGAGTGTGATGTTCTGTA 940
 Qy 1037 AGCAAGTGAAGCGGCGCTGATG 1059
 Db 941 AGCAAGTGAAGCGGCGCTGATG 963


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Db      |||||
52  TCTGTGGAGTGGAGCCCTTGGAGAGCCCTGTGTGCTGCGCCCTGGCAGAGCTCACAGCC 111
Qy      61  CCACCGCTGCTACTGAAAGCCCAAGGCTGTGAGACAGCTTCTCTTGGACCTTCTCTGG 120
Db      112  CCACCGCTGCTACTGAAAGCCCA-GGCTGTGAGACAGAGCTTCTCTTGGACCTTCTCTGG 170
Qy      121  CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCATGTGGTGAAGTGAAGCTTCAAGAGT 180
Db      171  CCTTAAAGGAGTGGGAGAGGCTTCCAGAGCATGTGGTGAAGTGAAGCTTCAAGAGT 230
Qy      181  CCTCCACCATGAGTGTGAAGTTCCTGGGAGGAGGACAGAGCTGTTTGTCTGACCTC 240
Db      231  CTTCCACCATGAGTGTGAAGTTCCTGGGAGGAGGACAGAGCTGTTTGTCTGACCTC 289
Qy      241  GTTACCTTTCACTGAGACAGAGCAAGTCCCGCTTCAAGATCCAGGGGAGAAACAGGG 300
Db      290  GTTACCTTTCACTGAGACAGAGCAAGTCCCGCTTCAAGATCCA-GGGAGAGAACAGGCG 348
Qy      301  GTTCCAGAGGCGCGGCTGTGAGTACCGTGGGCTGTGGGACCATCTGACCATGCTG 360
Db      349  GTTCCAGAGGCGCGGCTGTGAGTACCGTGGGCTGTGGGACCATCTGACCATGCTG 408
Qy      361  CGGACTGAGAGTCCCTGACAGCCCTTCAATGGGCTGTGGCGGCTTGAAGGCGCAGAT 420
Db      409  CGGACTGAGAGTCCCTGACAGCCCTTCAATGGGCTGTGGCGG-CTGAGAGGCGCAGAT 467
Qy      421  AGCTTGGCTTCACTGAGTCCGCTCTTATGACTCCGTCAAGAGGTGTACACCCCA- 479
Db      468  AGCTTGGCTTCACTGAGTCCGCTCTTATGACTCCGTCAAGAGGTGTACACCCCAAG 527
Qy      480  AGGCGGCGAGCACTCC 495
Db      528  AGGCGGCGAGCACTTC 543

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RESULT 13
LOCUS   CK025514
DEFINITION AGENCOURT_16618893 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7050849
5', mRNA sequence.
ACCESSION CK025514
VERSION   CK025514.1 GI:38551438
KEYWORDS EST.
SOURCE   Danio rerio (zebrafish)
ORGANISM Danio rerio
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
          Cypriniformes; Cyprinidae; Danio.
          1 (bases 1 to 1181)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: dsgerha@mail.nih.gov
          Tissue Procurement: Len Zon, Harvard
          cDNA Library Preparation: Open Biosystems
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHAM14822 row: 9 column: 07
          High quality sequence stop: 842.
          Location/Qualifiers
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              /mol_type="mRNA"
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/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tübingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH_ZGC_7). Library was constructed by Open Biosystems
(Huntsville, AL)."

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Query Match 34.4%; Score 423; DB 14; Length 1181;
Best Local Similarity 69.6%; Pred. No. 5,2e-84;
Matches 605; Conservative 0; Mismatches 255; Indels 9; Gaps 2;

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Db      66  CGCTGAGACAGGCGCAAGTCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCGG 125
Qy      311  CCGGCGTGTGAGTACGAGTCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCGG 370
Db      126  CTAAAGGAGTCCGCTTCAAGATCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCG 185
Qy      371  GTCCCTGAGAGCCCTTCAAGATCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCG 430
Db      186  GTCCGCGTCCGCTTCAAGATCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCG 245
Qy      431  CCAATCCGATCCGCTTCAAGATCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCG 490
Db      246  CCAATCCGATCCGCTTCAAGATCCGCTTCAAGATCCAGGGGAGAAAGCGGTTCAGAGCG 302
Qy      491  ACTCCAGAGCTCACTACCGGAGTTCGCGGCTGACAGAGAGGAGGAGGAGGAGGAGG 550
Db      303  ACCCTTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362
Qy      551  GTGCCAGGCGCAAGATGAGTGAAGTCCGATTCAGGCGCAGATCACTTGGGCGCAT 610
Db      363  TGGCTCAGGCGCAAGATGAGTGAAGTCCGATTCAGGCGCAGATCACTTGGGCGCAT 418
Qy      611  CCAAGAGCAGAGAAATACAGCGGAGCTATGAGAGGCTTACAGAACATGCGCAGGAGG 670
Db      419  --GGTGTGGAGAGAGATCAACAGGAGCAGATCAGGCGCAGATCTTCCAGCTTG 476
Qy      671  AAGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
Db      477  AAGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 536
Qy      731  ACTGCTGAGTGTGAGTCTGAGATCCATCAAGAGGAGGAGGAGGAGGAGGAGGAGG 790
Db      537  ACTGCTGAGTGTGAGTCTGAGATCCATCAAGAGGAGGAGGAGGAGGAGGAGGAGG 596
Qy      791  TCACTGACAACTTCCCTGCACTTGTCTGTGCTTGGAGCGGCTTGTGCTGACAG 850
Db      597  TGTGACAGAACTTCCCTGCACTTGTGTGTGCTTGGAGCGGCTTGTGCTGACAG 656
Qy      851  TGTGAGCGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 910
Db      657  TGTGAGCGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716
Qy      911  ACTTCAAGCCCTGCACTGATGATGAAGATGAGTGGCCAGAGAGGAGGAGGAGGAGG 970
Db      717  AAGAGAGTCTCAACAACTGCGCTGAGCATGTGCTAAAGAGGAGGAGGAGGAGGAGG 776
Qy      971  ACAAGGATTTACACCTCTTTTGTGCTTGGAGTCTGGAACGTGTGATGTTCTTGA 1030
Db      777  ACAAGGATTTGTCCGCTATCTGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 836

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QY 1031 CCTATGAGCAGCTGAAACGGGCGCTGATG 1059
 DB 837 CCTTTGAGCAGCTCAACGGGCGATGATG 865

RESULT 14
 AV413338 930 bp DNA linear GSS 17-DEC-2003
 LOCUS AV413338
 DEFINITION Pan troglodytes UCP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AV413338
 VERSION AV413338.1 GI:39769300
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE 1 (bases 1 to 930)
 Authors Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Title Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Journal Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 930)
 Authors Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Title Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 Comment This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 source location/Qualifiers
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 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
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ORIGIN
 Query Match 34.2%; Score 420.8; DB 29; Length 930;
 Best Local Similarity 63.9%; Pred. No. 1.5e-83;
 Matches 602; Conservative 0; Mismatches 325; Indels 15; Gaps 3;

QY 154 ATGGTTGAGTGAAGCCTTGAACCTGCTCCCAACCATGCTGTGAAGTTCTGGGGGCA 213
 DB 1 ATGGTTGGTTCAAGGCGCACAGATGCCCCCTACCTGCCACTGTGAAGTTCTTGGGACT 60

QY 214 GGCACAGCAGCTGTTTGTGCTGACCTGTTACCTTTCCATGTCACAGCCAAAGTCGCG 273
 DB 61 GGCACAGCTGCTGCTGACCTGACATCATCACTTCTCTGATATCGTGAAGTCGCG 120

QY 274 CTGCAGATCCAGGGGGAAGAACGAGG---CGGTCCAGACGCGCCGCTGTGCACTACCGT 330
 DB 121 TTACAGATCCAGGAGAAAGTCAAGGGGCAAGTGGCGCTACAGCCAGCGCCAGTACCGC 180

QY 331 GGCCTGTGCGACCAATCCCTGACATGATGTCGACCTGAGGGTCCCTGAGCCCTTACAT 390
 DB 181 GGTGTGATGGGACCAATTCGACATGATGTCGACCTGAGGGGCCCCGAGGCTTACAT 240

QY 391 GGGCTGTGCGCCGCTGACAGCCGACAGTGAAGCTTCCCTTCATCCGATCGGCTCTAT 450
 DB 241 GGGCTGTGCGCCGCTGACAGCCGACAGTGAAGCTTTCCTGTCGCGATCGGCTGAT 300

QY 451 GACTTCGTCAAGCAGGTATACACCCCGCAAGGCGGACCACTCAGCTCACTACCCG 510

DB 301 GATTCTGTCAACAGTCTTACA---CCAGGCGCTGTAGCANNNNNNNNNNNNNNNNNN 357
 QY 511 ATTTGGCGGCTGTCAGCACAGAGCCATGCGGTGACCTGTGCCAGCCACAGATGTG 570
 DB 358 NNN 417

QY 571 GTGAAGTTCGATTTTCAGGCCAGCATPACCTCGGCCATCCAGAGGACAGAAATTC 630
 DB 418 NNNNAGTCCGATTCAGG-----TCAGGCCCGGCTGAGAGGTGTGAGATAC 468

QY 631 ACCGGACCTATGAGAGCCCTPACAGAACATGCGCAGAGGAGAGAGTCAAGGCTGTG 690
 DB 469 CAAGGACCGTAAAGNNNTACAGAGCATTTGCCAGAGAGAGGTTCCGGGGCTCTGG 528

QY 691 AAAGGAACTTTGGCCCAACATCATGAGAAATGCTATGTCACCTGTGCTAGGTGTGACC 750
 DB 529 AAAGGAACTTCCCAATGTTGCTGTATGTCATTTGTCATGTCGAGCTGTGAGAGAC 588

QY 751 TACGATCTCTCAAGAGAAAGTGTGCTGACCTACACCTGCTCATGACAACTTCCCTGC 810
 DB 589 TATGACCTCATAGAGATGCTCTCTGAAAGCCACCTCATATACAGNNNNNTCCCTTGC 648

QY 811 CACTTTGTCTGCTGCTTTGAGACCGGCTTCTGTGCAACAGTGTGCTCCCGGTGAC 870
 DB 649 CACTTCACTTCTGCTTTGGGCGAGGCTTCTGACACCATGTATGCTCCCTGTAGAC 708

QY 871 GTGTGAGAACCCGGTATATGAACTCACTCAAGCCAGTACTTCAAGCCCTTCACTGT 930
 DB 709 GTGTGAGAACAGATATCATGAACTCTGCGGCGCACTATCATGAGCTGTGACCTGT 768

QY 931 ATGATTAAGATGTGCGCCAGAGAGGCGCCACAGCTTCTACAGAGATTTACACCTCC 990
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QY 991 TTTTTCGTTTGGGATCTGGAACGTGTGATGTTGTGAACCTATGAGCAGCTGAACCG 1050
 DB 829 TTTTTCGCTTGGGTTCTTGGGACGTTGTGATGTTGTGACCTATANNNTGAACGA 888

QY 1051 GCCCTGATGAAGTCCAGATGTTACGGGAATCACTTTTGA 1092
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RESULT 15
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 LOCUS B1248501
 DEFINITION 602992916F1 NCI_CGAP_Mams Mus musculus cDNA clone IMAGE:5148915 5',
 mRNA sequence.
 ACCESSION B1248501
 VERSION B1248501.1 GI:14794652
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 927)
 Authors NIH-MGC <http://mgc.nci.nih.gov/>.
 Title National Institutes of Health, Mammalian Gene Collection (MGC)
 Journal Unpublished (1999)
 Comment Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 919.
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 /clone_1b="NCI CGAP Mam5"
 /note="Organ: mammary; Vector: pCMV-Sport6; Site 1: Salt;
 Site 2: Not; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

ORIGIN

Query Match 32.9%; Score 405.4; DB 12; Length 927;
 Best Local Similarity 71.8%; Pred. No. 4.1e-80;
 Matches 605; Conservative 0; Mismatches 221; Indels 17; Gaps 5;

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274 CTGCAGATCCAGGGGAGAACAGCGC---GTCCAGACGGCCCGGCTCTGTCACTACCT 330
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67 CTGCAGATCCAGGGGAGAGTCAAGGGCTAAGTGGCAGCAGCCAGCCAGTACCT 126
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331 GGGGTCTGGGACCATCTGACATGATGGAGTGAAGGCTCCCTGACAGCCCTCAAT 390
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364 GTAAAGTCCGCTTCAAGC-----TCAGGCCGCGGCTGTGTGTGCGAGATAC 414
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631 AGCGGACTATGAGCGCTACAGAACCATGCGCAGAGGAGAGAGTCAAGGGCTGTGG 690
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415 CAGAGCATGTGCAAGCCTTACAGACCATTTGACAGAGAGAGAGATCCCGGGCTCTGG 474
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691 AAAGGAATTTGGCCCAACATCATGAGGAATGCTATGCTCAAGTGTGAGGTGA-C 749
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Db 775 CTTTCCGCTTGGATCTGG-ACGTAGTATGTTTGCACCTATGAGCAGTCAAAAG 833
 Qy 1050 GGC 1052
 Db 834 GCC 836

Search completed: May 18, 2004, 14:45:31
 Job time : 3081 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 06:43:51 ; Search time 525 Seconds
(without alignments)
9661.013 Million cell updates/sec

Title: US-09-423-410-3

Perfect score: 1231
Sequence: 1 tcccgagatgagccctagg.....ttgtcgcgtcaagaac 1231

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1231 | 100.0 | 1231 | 2 | AAV72690 Human unc |
| 2 | 1231 | 100.0 | 1231 | 6 | ABQ72999 CDN |
| 3 | 1202.2 | 97.7 | 2340 | 2 | AAV84254 Human unc |
| 4 | 1185.2 | 96.3 | 1220 | 2 | AAV71710 Human unc |
| 5 | 1146.4 | 93.1 | 1193 | 3 | AAZ46055 CDNA enco |
| 6 | 1146.4 | 93.1 | 1193 | 4 | AAZ46055 CDNA enco |
| 7 | 1146.4 | 93.1 | 1193 | 6 | AAZ46055 CDNA enco |
| 8 | 1145 | 93.0 | 1175 | 3 | AAZ29245 Human unc |
| 9 | 1144.8 | 93.0 | 1193 | 2 | AAV54602 Human unc |
| 10 | 1010.8 | 82.1 | 1032 | 2 | AAV72691 Human unc |
| 11 | 981.4 | 79.7 | 1132 | 3 | AAZ29324 Human unc |
| 12 | 981.4 | 79.7 | 1132 | 5 | AAZ14820 Human unc |
| 13 | 981.4 | 79.7 | 1132 | 5 | AAZ14820 Human unc |
| 14 | 981.4 | 79.7 | 1132 | 5 | AAZ14820 Human unc |
| 15 | 981.4 | 79.7 | 1132 | 6 | AAZ14820 Human unc |
| 16 | 967.8 | 78.6 | 1033 | 2 | AAV71711 Human unc |
| 17 | 939 | 76.3 | 939 | 2 | AAZ19969 Human unc |
| 18 | 939 | 76.3 | 939 | 4 | AAH18849 Human unc |
| 19 | 934.4 | 75.9 | 936 | 2 | AAV84745 Human unc |
| 20 | 732 | 59.5 | 1658 | 2 | AAV84307 Mouse unc |
| 21 | 732 | 59.5 | 2782 | 2 | AAZ07060 Mouse unc |
| 22 | 732 | 59.5 | 2782 | 2 | AAV71227 CDNA enco |
| 23 | 732 | 59.5 | 2782 | 3 | AAZ90318 CDNA enco |

| | | | | | |
|----|-------|------|------|---|--------------------|
| 24 | 732 | 59.5 | 2782 | 4 | AAZ09318 Mouse unc |
| 25 | 730.4 | 59.3 | 1204 | 2 | AAV71712 Mouse unc |
| 26 | 708.2 | 57.5 | 1215 | 9 | ADBS2719 Primary r |
| 27 | 705.4 | 57.3 | 1949 | 2 | AAZ07061 Mouse unc |
| 28 | 705.4 | 57.3 | 1949 | 2 | AAV71228 CDNA enco |
| 29 | 705.4 | 57.3 | 1949 | 3 | AAZ90319 CDNA enco |
| 30 | 705.4 | 57.3 | 1949 | 3 | AAZ90319 CDNA enco |
| 31 | 593.8 | 48.2 | 1777 | 2 | AAZ07062 Mouse unc |
| 32 | 593.8 | 48.2 | 1777 | 2 | AAV71229 CDNA enco |
| 33 | 593.8 | 48.2 | 1777 | 3 | AAZ90320 CDNA enco |
| 34 | 593.8 | 48.2 | 1777 | 3 | AAZ90320 CDNA enco |
| 35 | 490 | 39.8 | 1575 | 6 | ABK63772 Rat seque |
| 36 | 490 | 39.8 | 1575 | 6 | ABK63772 Rat seque |
| 37 | 490 | 39.8 | 1575 | 9 | ABK63772 Rat seque |
| 38 | 478.2 | 38.8 | 1612 | 7 | ADBS8373 Toxicity- |
| 39 | 476.6 | 38.7 | 1105 | 2 | AAV44595 Human res |
| 40 | 476.6 | 38.7 | 1105 | 2 | AAZ99434 UCP2 Nucl |
| 41 | 476.6 | 38.7 | 1105 | 2 | AAZ99434 UCP2 Nucl |
| 42 | 476.6 | 38.7 | 1105 | 3 | AAZ99434 UCP2 Nucl |
| 43 | 476.6 | 38.7 | 1105 | 5 | AAZ99434 UCP2 Nucl |
| 44 | 476.6 | 38.7 | 1596 | 2 | AAV82381 Human unc |
| 45 | 476.6 | 38.7 | 1596 | 3 | AAZ52254 Human unc |

ALIGNMENTS

| | | |
|----------|--|--------------------------|
| RESULT 1 | AAV72690 | standard; CDNA; 1231 BP. |
| ID | AAV72690 | standard; CDNA; 1231 BP. |
| XX | AAV72690; | |
| AC | AAV72690; | |
| XX | AAV72690; | |
| DT | 22-FEB-1999 | (first entry) |
| XX | 22-FEB-1999 | (first entry) |
| DE | Human uncoupling protein UCP3L encoding CDNA. | |
| XX | Human uncoupling protein UCP3L encoding CDNA. | |
| KW | Human: uncoupling protein; UCP3L; UCP3; oxidative phosphorylation; | |
| KW | adenosine triphosphate; mitochondria; skeletal muscle; gene therapy; | |
| KW | thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension; | |
| KW | insulin sensitivity; neuromuscular disease; ss. | |
| XX | Human sapiens. | |
| OS | Human sapiens. | |
| XX | Human sapiens. | |
| PH | Key | Location/Qualifiers |
| FT | CDS | 154..1092 |
| FT | | /*tag= a |
| FT | | /product= "UCP3L" |
| XX | | |
| PN | W09850542-A1. | |
| XX | 12-NOV-1998. | |
| PD | 12-NOV-1998. | |
| XX | 05-MAY-1998; | 98WO-EP002645. |
| PF | 05-MAY-1998; | 98WO-EP002645. |
| XX | 07-MAY-1997; | 97CH-00001072. |
| PR | 07-MAY-1997; | 97CH-00001072. |
| XX | | |
| PA | (NOVS) NOVARTIS AG. | |
| PA | (NOVS) NOVARTIS-ERFINDUNGEN VERM GBS MBH. | |
| XX | | |
| PI | Giacobino J, Muzzin P, Boss O; | |
| XX | | |
| DR | WPI, 1998-610382/51. | |
| XX | P-PSDB; AAW63379. | |
| XX | | |
| PT | New human skeletal muscle uncoupling protein UCP3L and UCP3S - useful | |
| PT | for controlling thermogenesis in human skeletal muscle and heart, e.g. | |
| PT | for treating obesity and cachexia. | |
| XX | | |
| PS | Claim 1, Page 14-15; 26pp: English. | |
| XX | | |
| CC | The present sequence encodes human uncoupling protein UCP3L. UCP3 | |
| CC | uncouples oxidative phosphorylation and synthesis of adenosine | |

triphosphate in the mitochondria of skeletal muscle. The coding sequences for UCP3L and UCP3S are useful for gene therapy of dysfunctions of thermogenesis in human skeletal muscle and heart which result from a lack of UCP3 and which can induce disorders such as obesity or cachexia. Antisense oligonucleotides to UCP3L and UCP3S can be used for correcting an excess of UCP3. Modification of endogenous UCP3 activity (using activators or inhibitors of UCP3) is used to induce bodyweight loss (loss of adipose mass and maintenance of the lean mass) in all types of obesity by promoting the dissipation of energy; for preventing an excessive weight regain following restrictive food diet or after ceasing a physical training programme; for preventing and treating type II diabetes by improving sensitivity to insulin; for preventing hypertension; for increasing muscle mass in states of cachexia; for treatment of insufficiencies or disturbances of cardiac rhythm due to a dysfunction of UCP3; and for the treatment of neuromuscular diseases due to a dysfunction of UCP3. The uncoupling proteins can also be used to raise antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows generation of transgenic animals, e.g. for screening substances which modify UCP3 expression or activity or for investigating the biological role of UCP3

Sequence 1231 BP; 271 A; 371 C; 345 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 1231; DB 2; Length 1231;

Best Local Similarity 100.0%; Pred. No. 3,5e-295; Indels 0; Gaps 0;

Matches 1231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCCTGGATGAGCCCTAGAGAGCCCTGTGCTGCTCCCTGCGAGAGACTACAGCC 60
 1 TCCTGGATGAGCCCTAGAGAGCCCTGTGCTGCTCCCTGCGAGAGACTACAGCC 60
 61 CCAAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGCTCTCTTGTGAGACTCTCTG 120
 61 CCAAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGCTCTCTTGTGAGACTCTCTG 120
 121 CCTTAAGGAGCTGGGAGAGAGCTTCCAGAGACTAGTGTGAGAGCTTCAAGCTTCA 180
 121 CCTTAAGGAGCTGGGAGAGAGCTTCCAGAGACTAGTGTGAGAGCTTCAAGCTTCA 180
 181 CCTCCACCATGCTGTGAGAGCTTCTGGGAGAGAGAGAGAGAGCTTCTTGTGAGCT 240
 181 CCTCCACCATGCTGTGAGAGCTTCTGGGAGAGAGAGAGAGAGCTTCTTGTGAGCT 240
 241 GTTACCTTTTCACTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 241 GTTACCTTTTCACTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 301 GTCCAG 360
 301 GTCCAG 360
 361 CGAGTGAAG 420
 361 CGAGTGAAG 420
 421 AGCTTGGCTCTCAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 421 AGCTTGGCTCTCAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 481 GGGGAG 540
 481 GGGGAG 540
 541 GCGGTGACCTGTGCGCCAGCCAGAGATGTGTGAGAGAGAGAGAGAGAGAGAGAG 600
 541 GCGGTGACCTGTGCGCCAGCCAGAGATGTGTGAGAGAGAGAGAGAGAGAGAGAG 600
 601 CTGGGAG 660
 601 CTGGGAG 660
 661 GCCAGGAG 720
 661 GCCAGGAG 720

661 GCCAGGAG 720
 721 GCTATCCGACCTGTGAG 780
 721 GCTATCCGACCTGTGAG 780
 781 TACCACTGCTCACTGAG 840
 781 TACCACTGCTCACTGAG 840
 841 TGTGCGACAG 900
 841 TGTGCGACAG 900
 901 CCAAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 901 CCAAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 961 ACAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 961 ACAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 1021 ATGTTGCTGACCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 1021 ATGTTGCTGACCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 1081 TCAAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 1081 TCAAGCGTGCATGAAAGCCAGGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 1141 AATGAG 1200
 1141 AATGAG 1200
 1201 CTGTTGTTACTTGTGCTGATTAAGAAAC 1231
 1201 CTGTTGTTACTTGTGCTGATTAAGAAAC 1231

RESULT 2
 AB072999
 ID AB072999 standard; cDNA, 1231 BP.
 XX
 AC AB072999;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DE UCP3L cDNA clone nucleotide sequence.
 XX
 KW UCP3L; UCP3S; diabetes; obesity; diabetic related condition; GMP;
 KW gene therapy; antidiabetic; anorectic; cardiant; nephrotropic; GK;
 KW antilipemic; blood glucose; glucokinase; regulatory protein; liver;
 KW glucokinase; hepatic triglyceride accumulation; fibrinogen; HDL;
 KW hepatic fatty acid oxidation; high density lipoprotein; cholesterol;
 KW glucose; gestational diabetes; hyperglycemic related disorder;
 KW kidney related disorder; cardiovascular disorder; gene; ss.
 XX
 OS Unidentified.
 XX
 FT Key
 FT CDS 154..1092
 FT FT /tag= a
 FT FT /product= "UCP3L protein"
 XX
 XX US2002065239-A1.
 PD 30-MAY-2002.
 XX
 XX 14-MAR-2001, 2001US-00808457.
 PF 15-MAR-2000, 2000US-0266328P.
 PR (CAPL/) CAPLAN S. L.
 XX
 XX

US 6628032,

QY 1141 AATGAGAGAAAAAGGTGATCCACGACACATGACAGACCCACACAT 1190
 DB 1171 AATGAGAGAAAAAGGTGATCCACGACACATGACAGACCCACACAT 1220

RESULT 5
 AA246055
 ID AA246055 standard; cDNA, 1193 BP.

XX AA246055;

XX 25-APR-2000 (first entry)

XX cDNA encoding a human uncoupling protein designated HHFCW60.

XX Human; HHFCW60; mitochondrial uncoupling protein family; muscle wasting;
 KM uncoupling protein; wound; tissue repair; inflammation; cachexia; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FH 199.1137
 XX CDS /*tag= a
 /product= "uncoupling protein"

XX W0200002577-A1.

XX 20-JAN-2000.

XX 02-DEC-1998; 98WO-EP007802.

XX 09-JUL-1998; 98GB-00014926.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Clapham JC, Beeley LJ, Godden RJ;

XX WPI; 2000-147542/13.

XX P-PsDB; AAY54600.

XX Use of uncoupling protein, polynucleotide and compound activating it, in
 PT treating wounds, inflammation, tissue repair, muscle wasting, and
 PT cachexia.

XX Claim 9; Page 21; 29pp; English.

XX The present sequence encodes a HHFCW60 polypeptide, which is a member of
 CC the mitochondrial uncoupling protein family. The HHFCW60 polynucleotide
 CC has homology with human uncoupling protein 2. The polynucleotide sequence
 CC was isolated from a cDNA library derived from human skeletal muscle cell
 CC mRNA, and mRNA from the cell lines rhabdomyosarcoma, caski, and SHSY 5Y. The
 CC protein is useful in producing antibodies and in screening for antagonist
 CC and agonist. The polynucleotide is useful as a reagent for diagnosing and
 CC determining susceptibility to the disease by detecting the mutation in
 CC the HHFCW60 gene. The polynucleotide, protein, and antibodies against
 CC HHFCW60 are useful in screening for the compounds that have an effect on
 CC the production of mRNA and polypeptides in the cell. These compounds are
 CC used to treat wounds, tissue repair, inflammation, muscle wasting or
 CC cachexia

XX Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;

XX Query Match 93.1%; Score 1146.4; DB 3; Length 1193;
 XX Best Local Similarity 99.9%; Pred. No. 3.3e-274;
 XX Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCTGGATGAGAGCCCTAGAGAGCCCTGTGCTGCCCTGCGTGCAGAGCTCACAGCC 60

DB 46 TCCTGGATGAGAGCCCTAGAGAGCCCTGTGCTGCCCTGCGTGCAGAGCTCACAGCC 105

QY 61 CCACCGCTGCACTGAAGCCAGGAGCTGTGAGAGAGCTCTCTCTTGGAGCTCTCTCGG 120

DB 106 CCACCGCTGCACTGAAGCCAGGAGCTGTGAGAGAGCTCTCTCTTGGAGCTCTCTCGG 165

QY 121 CCTTAAAGGAGCTGGGAGAGAGCCCTTCCAGAGCTATGTTGAGCTGAAGCCTTCAAGCTG 180
 DB 166 CCTTAAAGGAGCTGGGAGAGAGCCCTTCCAGAGCTATGTTGAGCTGAAGCCTTCAAGCTG 225

QY 181 CCTTCCACCATGCTGTGAAGTTCTTGGGGGACAGACAGAGCTGTTTGGTGAAGCTC 240

DB 226 CCTTCCACCATGCTGTGAAGTTCTTGGGGGACAGACAGAGCTGTTTGGTGAAGCTC 285

QY 241 GTTACCTTTCACTGAGACAGAGAGGTCGCTGTCAGATTCAGGGGAGAGACAGAGCG 300

DB 286 GTTACCTTTCACTGAGACAGAGAGGTCGCTGTCAGATTCAGGGGAGAGACAGAGCG 345

QY 301 GTCCAGAGAGCCGAGCTGTGTCAGTACCGTGGCTGTGAGCCATCTTGAACATGTTG 360

DB 346 GTCCAGAGAGCCGAGCTGTGTCAGTACCGTGGCTGTGAGCCATCTTGAACATGTTG 405

QY 361 CGAGCTGAGAGGTCCTGTGAGAGCCCTTCAATAGGCTGTGTGGCCGAGCTGACAGGCAATG 420

DB 406 CGAGCTGAGAGGTCCTGTGAGAGCCCTTCAATAGGCTGTGTGGCCGAGCTGACAGGCAATG 465

QY 421 AGCTTGGCTGCATCCGATGGGCTCTATGACTCCGTCAGAGAGGTATACCCCAAA 480

DB 466 AGCTTGGCTGCATCCGATGGGCTCTATGACTCCGTCAGAGAGGTATACCCCAAA 525

QY 481 GAGCGGAGCAACTCCAGGCTGACTTACCCGATTTTGGCCGCTGACCAAGAGCCATG 540

DB 526 GAGCGGAGCAACTCCAGGCTGACTTACCCGATTTTGGCCGCTGACCAAGAGCCATG 585

QY 541 GCGGTGACCTGTGTCAGAGCCCAAGATGTTGTTGAGAGGTCGATTTTCAAGGCAATAC 600

DB 586 GCGGTGACCTGTGTCAGAGCCCAAGATGTTGTTGAGAGGTCGATTTTCAAGGCAATAC 645

QY 601 CTCGGGACATCCAGAGAGGAGCAAGAAATATACAGCGGATATAGAGCTTACAGAAACAATC 660

DB 646 CTCGGGACATCCAGAGAGGAGCAAGAAATATACAGCGGATATAGAGCTTACAGAAACAATC 705

QY 661 GCCAGAGAGAGAGAGAGTCAAGGAGCTGTGAAAGAACTTTGCCCAATCATATAGAGAT 720

DB 706 GCCAGAGAGAGAGAGAGTCAAGGAGCTGTGAAAGAACTTTGCCCAATCATATAGAGAT 765

QY 721 GCTATGCTCACTGCTGAGAGTGTGACTTACAGCATCTCTCAAGAGAGAGCTGTGAC 780

DB 766 GCTATGCTCACTGCTGAGAGTGTGACTTACAGCATCTCTCAAGAGAGAGCTGTGAC 825

QY 781 TACCACTGCTCACTGAGCAACTTCCCTGCGCACTTGTCTCTGCTTGGAGCCGAGCTTC 840

DB 826 TACCACTGCTCACTGAGCAACTTCCCTGCGCACTTGTCTCTGCTTGGAGCCGAGCTTC 885

QY 841 TGTGTCACAGTGTGAGCTTCCCGGTGAGAGCTGTGAAAGACCCGGTATATGAATCACTC 900

DB 886 TGTGTCACAGTGTGAGCTTCCCGGTGAGAGCTGTGAAAGACCCGGTATATGAATCACTC 945

QY 901 CCAGGCTGATCTTCAAGCCCTTCCCTGCACTGTATGATTAAGTGTGGCCAGAGAGGAGCC 960

DB 946 CCAGGCTGATCTTCAAGCCCTTCCCTGCACTGTATGATTAAGTGTGGCCAGAGAGGAGCC 1005

QY 961 ACAGCTTCTCAAGAGATTTTACACCTCTCTTTTGGCTTGGAGTCTGTGAACGTGTG 1020

DB 1006 ACAGCTTCTCAAGAGATTTTACACCTCTCTTTTGGCTTGGAGTCTGTGAACGTGTG 1065

QY 1021 ATGTTGTAACCTATGAGAGCTGAAGAGGAGCCCTGATGAAGATTCAGATGTTTACGGAA 1080

DB 1066 ATGTTGTAACCTATGAGAGCTGAAGAGGAGCCCTGATGAAGATTCAGATGTTTACGGAA 1125

QY 1081 TCACGTTTGAACAAGCAAGAAGGCACTGTGTGCTTACAGTGTCCGAACCAAGTTAAG 1140

DB 1126 TCACGTTTGAACAAGCAAGAAGGCACTGTGTGCTTACAGTGTCCGAACCAAGTTAAG 1185

QY 1141 AATGGAAG 1148
 DB 1186 AATGGAAG 1193

RESULT 6

AAD08530

AAD08530 standard; cDNA; 1193 BP.

AAD08530;

04-SEP-2001 (first entry)

Human uncoupling protein-3 (UCP3) cDNA.

Human; UCP3; uncoupling protein-3; chromosome 11q13; gene therapy; atherosclerosis; hypercholesterolaemia; antilipemic; ss.

Homo sapiens.

Key Location/Qualifiers

199..1137

/tag= a

/product= "Human UCP3 protein"

MO200143760-A2.

21-JUN-2001.

18-DEC-2000; 2000MO-BP012931.

17-DEC-1999; 99GB-00030100.

(SMIK) SMITHKLINE BEECHAM PLC.

Clapham JC;

MPI: 2001-398073/42.

P-PSDB; AAE04298.

Use of a compound selected from UCP3 polypeptide, a compound which activates the polypeptide, or a polynucleotide encoding the polypeptide, for treating atherosclerosis or hypercholesterolaemia.

Claim 9; Page 19; 24pp; English.

The present sequence is a cDNA encoding human UCP3 (uncoupling protein-3) protein. UCP3 gene is located in chromosome 11q13. UCP3 protein and CC polynucleotides encoding them are useful for identifying agonist compounds which are potentially useful in therapy. UCP3 protein is useful for inducing an immunological response, as immunogen to produce antibodies immunospecific for UCP3 protein, and in a method for the structure-based design of an agonist of UCP3 protein. UCP3 sequences are useful to configure screening methods for detecting the effect of added components on the production of mRNA and polypeptide in cells. UCP3 DNA is used in gene therapy. A compound which activates UCP3 protein or a polynucleotide encoding UCP3 protein are used for the manufacture of a medicament for treating atherosclerosis or hypercholesterolaemia

Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;

Query Match 93.1%; Score 1146.4; DB 4; Length 1193;

Best Local Similarity 99.9%; Pred. No. 3.3e-274; Indels 0; Gaps 0;

Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCTGGATGAGACCTAGGAGCCCTGTGTGCTCCCTGCGTGGCAGAGCTCAGAGCC 60
 46 TCCTGGATGAGACCTAGGAGCCCTGTGTGCTCCCTGCGTGGCAGAGCTCAGAGCC 105
 61 CCACCGCTGCTGAGAGCCAGGCTGTGAGAGAGCTCTCTCTTGAAGCTCTCTCGG 120
 106 CCACCGCTGCTGAGAGCCAGGCTGTGAGAGAGCTCTCTCTTGAAGCTCTCTCGG 165
 121 CCTTAAGGAGCTGGGAGAGCCTTCAGAGCTATGTTGAGCTGAAGCTTCAGAGCTG 180
 166 CCTTAAGGAGCTGGGAGAGCCTTCAGAGCTATGTTGAGCTGAAGCTTCAGAGCTG 225

181 CTTCCACCAATGCTGTGAGATTTCTGGGGGCGAGGCAAGACCGCTGTTGCTGACCTC 240

226 CTTCCACCAATGCTGTGAGATTTCTGGGGGCGAGGCAAGACCGCTGTTGCTGACCTC 285

241 GTTACCTTTCATGAGACAGCCAGAGTCCGCTGACAGATCCAGGGGAGAACAGGCG 300

286 GTTACCTTTCATGAGACAGCCAGAGTCCGCTGACAGATCCAGGGGAGAACAGGCG 345

301 GTTCAGAGCGCCCGCTGTGAGTACCGTGGCGTGTCTGGGACCATCTGACATGTG 360

346 GTTCAGAGCGCCCGCTGTGAGTACCGTGGCGTGTCTGGGACCATCTGACATGTG 405

361 CGGACTGAGGGTCCCTGACAGCCCTTCAATAGGCTGTGTGCGGCTGTGAGGCGCAGATG 420

406 CGGACTGAGGGTCCCTGACAGCCCTTCAATAGGCTGTGTGCGGCTGTGAGGCGCAGATG 465

421 AGCTTGGCTTCATCGAGTGGGCTCTATGACTCGTCAAGAGTGTACACCCCAAA 480

466 AGCTTGGCTTCATCGAGTGGGCTCTATGACTCGTCAAGAGTGTACACCCCAAA 525

481 GCGGCGGACAACTCCAGCTCTACCTACCGGATTTTGGCGGCTGTGACCAAGAGCCATG 540

526 GCGGCGGACAACTCCAGCTCTACCTACCGGATTTTGGCGGCTGTGACCAAGAGCCATG 585

541 GCGGCGGACCTTGTGCGGACCGCCACAGATGTGTGAAAGTCCGATTTTCAAGGCGCAGATAC 600

586 GCGGCGGACCTTGTGCGGACCGCCACAGATGTGTGAAAGTCCGATTTTCAAGGCGCAGATAC 645

601 CTGGGGCCATCCAGAGGAGCAGAAAATACAGCGGAGCTATGAGACGCTACAGAAACATC 660

646 CTGGGGCCATCCAGAGGAGCAGAAAATACAGCGGAGCTATGAGACGCTACAGAAACATC 705

661 GCCAGGAGAGAAAGATCAAGGGGCTGTGAAAGAACTTTGCCCAATCATAGAGAAAT 720

706 GCCAGGAGAGAAAGATCAAGGGGCTGTGAAAGAACTTTGCCCAATCATAGAGAAAT 765

721 GCTATGTCACTGTGCTGAGGTGTGATCTACAGATCTCTCAAGAGAAAGCTGTGAGC 780

766 GCTATGTCACTGTGCTGAGGTGTGATCTACAGATCTCTCAAGAGAAAGCTGTGAGC 825

781 TACCACTGCTCAGACAGAACTTCCCTGCACTTTGTCTGTGCTTGGAGCGGCTTC 840

826 TACCACTGCTCAGACAGAACTTCCCTGCACTTTGTCTGTGCTTGGAGCGGCTTC 885

841 TGTGCCAGATGATGCTCCCGGTGAGCGTGTGAGAACCCGGTATATGAATCACTCCT 900

886 TGTGCCAGATGATGCTCCCGGTGAGCGTGTGAGAACCCGGTATATGAATCACTCCT 945

901 CCAGGCGAGTACTTCAAGCCCTTCACTGTATATATATATATATATATATATATATAT 960

946 CCAGGCGAGTACTTCAAGCCCTTCACTGTATATATATATATATATATATATATATAT 1005

961 ACAGCTTTCAGAGGAGTTTACACCTCTTTTGGCTTGGAGTCTGGAAGTGTG 1020

1006 ACAGCTTTCAGAGGAGTTTACACCTCTTTTGGCTTGGAGTCTGGAAGTGTG 1065

1021 ATGTTGTAACCTATGAGAGCTGAACCGGCGCTGATGAAGTTCAGAGTATTCAGGAA 1080

1066 ATGTTGTAACCTATGAGAGCTGAACCGGCGCTGATGAAGTTCAGAGTATTCAGGAA 1125

1081 TCACGCTTTTGAACAGACAGAAAGCCACTGTGTACTAACTGTGTCCGAACCAAGTTAAG 1140

1126 TCACGCTTTTGAACAGACAGAAAGCCACTGTGTACTAACTGTGTCCGAACCAAGTTAAG 1185

1141 AATGGAAG 1148

1186 AATGGAAG 1193

RESULT 7

AAD30499

AAD30499 standard; cDNA; 1193 BP.

XX

AC AAD30499;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Human mitochondrial uncoupling protein 3 (UCP3) cDNA.
 XX
 KW Human; mitochondrial uncoupling protein 3; UCP3; obesity; diabetes;
 XX body weight disorder; gene therapy; chromosome 11q13; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 199..1137
 FT /tag=a
 FT /product="Human UCP3 protein"
 FT
 PN WO20020754-A2.
 XX
 PD 31-JAN-2002.
 XX
 PE 25-JUL-2001; 2001WO-GB003341.
 XX
 PR 25-JUL-2000; 2000GB-00018248.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Clapham J;
 XX
 DR WPI; 2002-217023/27.
 DR P-Psdb; AAE19348.
 XX
 XX
 PT Use of mitochondrial uncoupling protein 3 polypeptide, polynucleotide and
 PT compounds which activate the polypeptide or polynucleotide for treating
 PT obesity, diabetes or body weight disorder.
 PS
 XX
 XX Claim 9; Page 18; 22pp; English.
 CC The present sequence is human mitochondrial uncoupling protein 3 (UCP3)
 CC encoding cDNA. The UCP3 gene is located on chromosome 11q13. UCP3
 CC sequences are used for identifying compounds which modulate their
 CC activity. They are used for the manufacture of a medicament for treating
 CC obesity, diabetes and body weight disorder. UCP3 sequences are also used
 CC in gene therapy
 CC
 SQ Sequence 1193 BP; 252 A; 369 C; 344 G; 228 T; 0 U; 0 Other;
 Query Match 93.1%; Score 1146.4; DB 6; Length 1193;
 Best Local Similarity 99.9%; Pred. No. 3.3e-274;
 Matches 1147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 361 CGA CTGAGGGTCCCTGACGCCCTTACATAGGCTGTGAGCGGCTTCAGCGCAGATG 420
 DB 406 CGA CTGAGGGTCCCTGACGCCCTTACATAGGCTGTGAGCGGCTTCAGCGCAGATG 465
 QY 421 AGCTTGCTTCATCCGCGATGAGCTTATGACTCCGTCAAGAGAGTGTACACCCCAAA 480
 DB 466 AGCTTGCTTCATCCGCGATGAGCTTATGACTCCGTCAAGAGAGTGTACACCCCAAA 525
 QY 481 GCGCGGACAACTCAGCTTCACTACCGGATTTTGGCCGGCTGACCAACAGAGCCATG 540
 DB 526 GCGCGGACAACTCAGCTTCACTACCGGATTTTGGCCGGCTGACCAACAGAGCCATG 585
 QY 541 GCGGTGACCTGTGCCAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGCTACAC 600
 DB 586 GCGGTGACCTGTGCCAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGCTACAC 645
 QY 601 CTCGGGCCATCAGAGAGGACAGAAAATACAGCGGAGCTATGAGCGCTTACAGAACATC 660
 DB 646 CTCGGGCCATCAGAGAGGACAGAAAATACAGCGGAGCTATGAGCGCTTACAGAACATC 705
 QY 661 GCCAGGAGAGAGAGTCAAGGGGCTGTGAGAAAGAACTTTGGCCCAATCATATAGAGAT 720
 DB 706 GCCAGGAGAGAGAGTCAAGGGGCTGTGAGAAAGAACTTTGGCCCAATCATATAGAGAT 765
 QY 721 GCTATGCTCAACTGTGCTGAGTGTGACTACGACATCTCTCAAGAGAGAGCTGTGAC 780
 DB 766 GCTATGCTCAACTGTGCTGAGTGTGACTACGACATCTCTCAAGAGAGAGCTGTGAC 825
 QY 781 TACCACTGCTCACTGACCAACTTCCCTGCACTTTGTCTGTGCTTTGAGCCGCTTC 840
 DB 826 TACCACTGCTCACTGACCAACTTCCCTGCACTTTGTCTGTGCTTTGAGCCGCTTC 885
 QY 841 TGTGCAAGAGTGTGCTCCCGGTGAGAGTGTGAGAGCCGGTATATAGACCTACCT 900
 DB 886 TGTGCAAGAGTGTGCTCCCGGTGAGAGTGTGAGAGCCGGTATATAGACCTACCT 945
 QY 901 CCAGGCGAGTACTCAGGCCCTCGACTGTATGATTAAGATGTGTGAGCCAGAGGGCCCTC 960
 DB 946 CCAGGCGAGTACTCAGGCCCTCGACTGTATGATTAAGATGTGTGAGCCAGAGGGCCCTC 1005
 QY 961 ACAGCTTCTCAAGAGATTTACACCTCTTTTGTGCTTTGGAGTCTGTGAACGTGTG 1020
 DB 1006 ACAGCTTCTCAAGAGATTTACACCTCTTTTGTGCTTTGGAGTCTGTGAACGTGTG 1065
 QY 1021 ATGTTCGTAACTTATGACAGCTGAAAGGGCCCTGAGAGAGTCAATGTACAGGAA 1080
 DB 1066 ATGTTCGTAACTTATGACAGCTGAAAGGGCCCTGAGAGAGTCAATGTGTACAGGAA 1125
 QY 1081 TCACGTTTGAACAAGAGAGGCACTGTGTATACGTGTCCGAAACCACTTAAG 1140
 DB 1126 TCACGTTTGAACAAGAGAGGCACTGTGTATACGTGTCCGAAACCACTTAAG 1185
 QY 1141 AATGGAAG 1148
 DB 1186 AATGGAAG 1193

RESULT 8
 AA229245
 ID AA229245 standard; cDNA; 1175 BP.
 XX
 XX AA229245;
 XX
 XX 28-FEB-2000 (first entry)
 XX
 DE Human mitochondrial anion carrier, uncoupling protein-3 cDNA.
 XX
 XX Mitochondrial uncoupling protein-3; UCP-3; mitochondrial anion carrier;
 KW MAC; modulator; transport protein; fatty acid anion; mitochondria;
 KW assay vesicle; metabolic disorder; diabetes; obesity; cancer; human; de.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 184..1122
FT /*tag= a
FT /product= "UCP-3"
XX
XX MO9964458-A1.
XX
XX 16-DEC-1999.
XX
XX 08-JUN-1999; 99WO-US012623.
XX
XX 08-JUN-1998; 98US-00093662.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Corkey BE, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;
XX
XX MPI; 2000-087200/07.
XX
XX P-PSDB; AAY44253.
XX
XX Identifying modulators of mitochondrial anion carriers, potentially
XX useful for treating metabolic disease, e.g. diabetes and obesity.
XX
XX Claim 11; Page 72-73; 80pp; English.
XX
XX The present sequence is a cDNA encoding human uncoupling protein-3 (UCP-
XX 3) which is a mitochondrial anion carrier (MAC). The UCPs transport free
XX fatty acid anions across the inner mitochondrial membrane to induce
XX cyclical proton movement. This transport is tightly related to oxidation
XX of fatty acids in the mitochondria, thereby converting fatty acids into
XX energy rather than storing them. The uncoupling protein is used in the
XX preparation of assay vesicles that are used to identify modulators of MAC
XX activity. MAC modulators are useful for treating metabolic disorders,
XX particularly diabetes and obesity. Modulators that act as inhibitors can
XX be used to treat conditions requiring a reduction in energy expenditure,
XX e.g. in cancer patients or the elderly
XX
XX Sequence 1175 BP; 248 A; 362 C; 337 G; 228 T; 0 U; 0 Other;
XX
XX Query Match 93.0%; Score 1145; DB 3; Length 1175;
XX Best Local Similarity 100.0%; Pred. No. 7,3e-274;
XX Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TCCTGGATGAGACCTTGAAGAGCCCTGCTGCTCCCTGCGTGGCAGAGCTCAGAGCC 60
XX 31 TCCTGGATGAGACCTTGAAGAGCCCTGCTGCTCCCTGCGTGGCAGAGCTCAGAGCC 90
XX 61 CCACCGCTGCTGAGAGCCCAAGGCTGTGAGAGAGCTCTCTCTTGAAGCTCTCTCG 120
XX 91 CCACCGCTGCTGAGAGCCCAAGGCTGTGAGAGAGCTCTCTCTTGAAGCTCTCTCG 150
XX
XX 121 CCCTAAAGGAGCTGGGCAAGCTTCCAGAGCTATGTTGAGACTGAAGCTTCCAGAGCTG 180
XX 151 CCCTAAAGGAGCTGGGCAAGCTTCCAGAGCTATGTTGAGACTGAAGCTTCCAGAGCTG 210
XX 181 CCCTAAAGGAGCTGGGCAAGCTTCCAGAGCTATGTTGAGACTGAAGCTTCCAGAGCTG 240
XX 211 CCCTAAAGGAGCTGGGCAAGCTTCCAGAGCTATGTTGAGACTGAAGCTTCCAGAGCTG 270
XX 241 GTTACCTTTCACTGAGACAGGCAAGGTCCTGCTGCTGAGATCCAGGGGAGAAACAGGCG 300
XX 271 GTTACCTTTCACTGAGACAGGCAAGGTCCTGCTGCTGAGATCCAGGGGAGAAACAGGCG 330
XX 301 GTTCCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
XX 331 GTTCCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390
XX 361 CGGACTGAGAGGCTGCTGAGAGCCCTTCAATAGGCTGATGAGCTGAGAGCTGAGAGT 420
XX 391 CGGACTGAGAGGCTGCTGAGAGCCCTTCAATAGGCTGATGAGCTGAGAGCTGAGAGT 450
XX 421 AGCTTGCTCCATCCGATCGGCTCTATGACTCCGTCAAGAGGATGTAACCCCAAA 480

DB 451 AGCTTGCTCCATCCGATCGGCTCTATGACTCCGTCAAGAGGATGTAACCCCAAA 510
XX
XX 481 GCGCGGAGCAATCCAGGCTCACTACCGGATTTTGGCGGCTGACCAAGAGGCTCATG 540
XX 511 GCGCGGAGCAATCCAGGCTCACTACCGGATTTTGGCGGCTGACCAAGAGGCTCATG 570
XX 541 GCGGTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
XX 571 GCGGTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 630
XX 601 CTGCGGCTCATCCAGAGGAGCAAGAAATATACGCGGAGCTATGAGAGCTGAGAGCATC 660
XX 631 CTGCGGCTCATCCAGAGGAGCAAGAAATATACGCGGAGCTATGAGAGCTGAGAGCATC 690
XX 661 GCGAGGAGAGAGAGTCAAGGAGGCTGTGAGAAAGGACTTTGCCCAATCATAGAGAT 720
XX 691 GCGAGGAGAGAGAGTCAAGGAGGCTGTGAGAAAGGACTTTGCCCAATCATAGAGAT 750
XX 721 GCTATGCTCACTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
XX 751 GCTATGCTCACTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 810
XX 781 TACCACTGCTCACTGAGACACTTCCCTGCGCACTTGTCTGCTGCTGCTGCTGCTGCTG 840
XX 811 TACCACTGCTCACTGAGACACTTCCCTGCGCACTTGTGTCTGCTGCTGCTGCTGCTGCTG 870
XX 841 TGTGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
XX 871 TGTGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
XX 901 CCAGGCGAGTACTTCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
XX 931 CCAGGCGAGTACTTCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
XX 961 AAGGCTTCTAAGAGGATTTACACCTCTTTTGGCTTGGAGTCTGAGAGCTGAGT 1020
XX 991 AAGGCTTCTAAGAGGATTTACACCTCTTTTGGCTTGGAGTCTGAGAGCTGAGT 1050
XX 1021 ATGTTCTGTAAGCTATGAGAGCTGAGAGGAGGCTGATGAAAGTCCAGATGTTACGGGAA 1080
XX 1051 ATGTTCTGTAAGCTATGAGAGCTGAGAGGAGGCTGATGAAAGTCCAGATGTTACGGGAA 1110
XX 1081 TCACGCTTTTGAACAAGACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
XX 1111 TCACGCTTTTGAACAAGACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1170
XX
XX 1141 AATGG 1145
XX 1171 AATGG 1175
XX
XX RESULT 9
XX AAV54602
XX ID AAV54602 standard; cDNA; 1193 BP.
XX
XX AAV54602;
XX
XX 07-DEC-1998 (first entry)
XX
XX Human uncoupling protein HNF1C60 cDNA.
XX
XX HNF1C60; uncoupling protein; human; body weight disorder; obesity;
XX diabetes; hyperlipidemia; diagnosis; therapy; vaccine; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 199..1137
XX /*tag= a
XX
XX MO9839432-A1.

PD 11-SEP-1998.
 XX 02-MAR-1998; 98MO-GB000633.
 XX 05-MAR-1997; 97GB-00004551.
 PR 18-MAR-1997; 97GB-00005614.
 PR 16-JUL-1997; 97EP-00305305.
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA Bealey LJ, Paine K, Godden RJ,
 XX WPI; 1998-495841/42.
 DR P-PSDB; AAM68197.
 PT New isolated human uncoupling poly(peptide)s - used to develop products
 PT for the diagnosis, prevention and treatment of body weight disorders,
 PT obesity and diabetes.
 XX
 PS Claim 3; Page 24-25; 41pp; English.
 XX
 CC This isolated polynucleotide (PN) codes for novel human uncoupling
 CC protein HNPCM60 (see AAM68197). HNPCM60 polynucleotides (see also
 CC AAY54603-04) can be obtained from a cDNA library derived from mRNA in
 CC cells of human brain frontal cortex, thadomyosarcoma, foetal heart and
 CC skeletal muscle using expressed sequence tag analysis. The invention
 CC relates to HNPCM60 polypeptides and recombinant materials and methods for
 CC their production. It also relates to methods for using such HNPCM60
 CC polypeptides and polynucleotides. Such uses include the treatment of
 CC obesity, diabetes, hyperlipidaemia and body weight disorders. The
 CC invention also provides methods to identify agonists and antagonists, and
 CC methods for treating conditions associated with HNPCM60 imbalance using
 CC the identified compounds. In addition, diagnostic assays for detecting
 CC diseases associated with inappropriate HNPCM60 activity or levels are
 CC provided
 CC
 CC Sequence 1193 BP; 252 A; 370 C; 343 G; 228 T; 0 U; 0 Other;
 SQ
 Query Match 93.0%; Score 1144.8; DB 2; Length 1193;
 Best Local Similarity 99.8%; Pred. No. 8.2e-274;
 Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TCCTGGAGTGAAGCCCTAGGAGAGCCCTGTGCTGCTCCCTGCGGAGAGACTCAAGCC 60
 DB 46 TCCTGGAGTGAAGCCCTAGGAGAGCCCTGTGCTGCTCCCTGCGGAGAGACTCAAGCC 105
 QY 61 CCAAGCGCTGCACTGAAGCCCAAGGCTGTGTGAGAGAGCTCTCTCTTGTGAGCTCTCTG 120
 DB 106 CCAAGCGCTGCACTGAAGCCCAAGGCTGTGTGAGAGAGCTCTCTCTTGTGAGCTCTCTG 165
 QY 121 CCTTAAGGAGACTGGGAGAGCCCTTCAAGACTATGATGATGAGTGAAGGCTTCAAGCTG 180
 DB 166 CCTTAAGGAGACTGGGAGAGCCCTTCAAGACTATGATGATGAGTGAAGGCTTCAAGCTG 225
 QY 181 CCTCCACCATGCTGTGTAAGTTCCTGAGGAGAGGAGAGAGCCCTGTTTGTGACCTC 240
 DB 226 CCTCCACCATGCTGTGTAAGTTCCTGAGGAGAGGAGAGAGCCCTGTTTGTGACCTC 285
 QY 241 GTTACTCTTTCACCTGAGACAGCCCAAGTTCCTGCTCAATTCAGGGGAGAAACCGAGG 300
 DB 286 GTTACTCTTTCACCTGAGACAGCCCAAGTTCCTGCTCAATTCAGGGGAGAAACCGAGG 345
 QY 301 GTTCAGAGAGGCGGCTGTGAGAGTACCGTGGGCTGTGAGGAGCACTCTGACCATGTG 360
 DB 346 GTTCAGAGAGGCGGCTGTGAGAGTACCGTGGGCTGTGAGGAGCACTCTGACCATGTG 405
 QY 361 CGGACTGAGAGTTCCTGAGAGCCCTTCAATGAGGCTGTGAGGCGGCTGAGAGCGCAGATG 420
 DB 406 CGGACTGAGAGTTCCTGAGAGCCCTTCAATGAGGCTGTGAGGCGGCTGAGAGCGCAGATG 465
 QY 421 AGCTTGCTCTCCATCCGAGATGCGGCTGTATGATCTCCGTCAGAGAGGTATACACCCCAAA 480
 DB 466 AGCTTGCTCTCCATCCGAGATGCGGCTGTATGATCTCCGTCAGAGAGGTATACACCCCAAA 525

QY 481 GCGCGGAGCAACTCCAGCTCACTACCCGGATTTTGGCGGCTGACCAAGAGCCATG 540
 DB 526 GCGCGGAGCAACTCCAGCTCACTACCCGGATTTTGGCGGCTGACCAAGAGCCATG 585
 QY 541 GCGGTGACCTGTGCGCCAGGCCCAAGATGTGTGAAGGTCGATTTTCAAGCCAGATACAC 600
 DB 586 GCGGTGACCTGTGCGCCAGGCCCAAGATGTGTGAAGGTCGATTTTCAAGCCAGATACAC 645
 QY 601 CTCGGGCAATCCAGAGAGGAGCAAGAAATATACAGCGGACTATGAGCGCTTACAGAACATC 660
 DB 646 CTCGGGCAATCCAGAGAGGAGCAAGAAATATACAGCGGACTATGAGCGCTTACAGAACATC 705
 QY 661 GCCAGAGAGAGAGAGTCAAGGAGGCTGTGAAAGAACTTTTGGCCCAATCATGTAGAGAT 720
 DB 706 GCCAGAGAGAGAGAGTCAAGGAGGCTGTGAAAGAACTTTTGGCCCAATCATGTAGAGAT 765
 QY 721 GCTATCGTCACTGTGCTGAGAGTGTGTGACTTACGATCTTCAAGAGAGAGTGTGAGC 780
 DB 766 GCTATCGTCACTGTGCTGAGAGTGTGTGACTTACGATCTTCAAGAGAGAGTGTGAGC 825
 QY 781 TACCACTGCTCACTGACCACTCCCTGCACTTGTCTGCTTGTGAGCCGAGCTTC 840
 DB 826 TACCACTGCTCACTGACCACTCCCTGCACTTGTCTGCTTGTGAGCCGAGCTTC 885
 QY 841 TGTGCAAGTGTGTGCTCTCCCGGTGAGCTGTGAAAGCCCGGTATATGAACTTCACT 900
 DB 886 TGTGCAAGTGTGTGCTCTCCCGGTGAGCTGTGAAAGCCCGGTATATGAACTTCACT 945
 QY 901 CCAAGCGCTACTTCCAGCCCTTCAAGTATGATGATGATGATGATGATGATGATGATGATG 960
 DB 946 CCAAGCGCTACTTCCAGCCCTTCAAGTATGATGATGATGATGATGATGATGATGATGATG 1005
 QY 961 ACAGCTTCTCAAGAGATTTTACACCTCTTTTTCGTTTGGATCTGTGAACCTGTGTG 1020
 DB 1006 ACAGCTTCTCAAGAGATTTTACACCTCTTTTTCGTTTGGATCTGTGAACCTGTGTG 1065
 QY 1021 ATGTTGTAACCTATGAGAGAGTGAACGAGGCTGTGATGAAGTCAAGATGTTACGGGAA 1080
 DB 1066 ATGTTGTAACCTATGAGAGAGTGAACGAGGCTGTGATGAAGTCAAGATGTTACGGGAA 1125
 QY 1081 TCACCGTTTGAACAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
 DB 1126 TCACCGTTTGAACAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1185
 QY 1141 AATGGAAG 1148
 DB 1186 AATGGAAG 1193
 RESULT 10
 AAX08507
 ID AAX08507 standard; DNA; 1022 BP.
 XX
 XX AAX08507;
 AC
 AC 19-JUL-1999 (first entry)
 DT
 DT
 XX
 XX
 DE Human UCP-3 (uncoupling protein) gene.
 KW UCP-3; uncoupling protein; thermogenesis; skeletal muscle; treatment;
 KW obesity; diabetes; hyperthermia; fever; detection; diagnosis; ss.
 OS
 OS Homo sapiens.
 XX
 XX
 PH Key Location/Qualifiers
 FT CDS 28..966
 FT /tag= a
 XX /product= "Uncoupling protein"
 XX
 XX
 PD MO9845313-A1.
 PD 15-OCT-1998.

XX PF 25-MAR-1998; 98MO-US005892.
 XX PR 04-APR-1997; 97US-0043407P.
 XX PR 08-MAY-1997; 97US-0046154P.
 XX PA (AMYL-) AMYLIN PHARM INC.
 XX PI Larkin S, Moore C, Albrandt K, Young A, Beaumont K;
 XX PR WPI: 1999-131682/11.
 XX DR P-PSDB; AAM85667.
 XX PT New isolated uncoupling protein, UCP3 - used to develop products for
 XX PT modulating thermogenesis in tissues, e.g. for treating obesity, diabetes,
 XX PT malignant hyperthermia or fever.
 XX PS Claim 5; Fig 5; 97pp; English.
 XX CC The uncoupling protein UCP-3 is involved in thermogenesis and energy
 XX CC utilization in skeletal muscle. The nucleic acid molecule encoding UCP-3
 XX CC or compounds which activate UCP-3 can be used to increase thermogenesis
 XX CC in a subject, e.g. for treating obesity or for decreasing the amount of
 XX CC fat in a subject. They can also be used for treating diabetes. Compounds
 XX CC which inhibit UCP-3 activation in tissues of a subject can be used for
 XX CC decreasing thermogenesis or respiratory ATP synthesis e.g. for preventing
 XX CC or treating malignant hyperthermia or fever. The UCP-3 can also be used
 XX CC for screening for compounds that bind to or modulate the activity of UCP-
 XX CC 3, these compounds can then be used in detection and diagnosis
 XX SQ Sequence 1022 BP; 228 A; 301 C; 292 G; 201 T; 0 U; 0 Other;

Query Match 82.1%; Score 1010.8; DB 2; Length 1022;
 Best Local Similarity 99.8%; Pred. No. 1.3e-240;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 GGCAGAGCCTTCAGACATATGTTGAGTGAAGCTTCAGAGCTTCCTCCACATGCG 194
 DB 9 GGCAGAGCCTTCAGACATATGTTGAGTGAAGCTTCAGAGCTTCCTCCACATGCG 68
 QY 195 TGTGAAGTTCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254
 DB 69 TGTGAAGTTCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 128
 QY 255 GGAACAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 314
 DB 129 GGAACAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 188
 QY 315 GCTGTGACAGTACCGGTGGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
 DB 189 GCTGTGACAGTACCGGTGGCTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 248
 QY 375 CTGACAGCCCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 434
 DB 249 CTGACAGCCCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 308
 QY 435 CCGCATCGGCTCTATGATCCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 494
 DB 309 CCGCATCGGCTCTATGATCCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 368
 QY 495 GAGCCTCACTACCCCGGATTTGGCCGGCTGACCAAGAGGAGGAGGAGGAGGAGGAGGAGG 554
 DB 369 GAGCCTCACTACCCCGGATTTGGCCGGCTGACCAAGAGGAGGAGGAGGAGGAGGAGGAGG 428
 QY 555 CCAAGCCCAAGATGTGTGAAGGTCGATTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 614
 DB 429 CCAAGCCCAAGATGTGTGAAGGTCGATTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 488
 QY 615 GAGCGACAGAAATATACAGCGGAGCTATGAGCGCTTACAGAAACATCCGCGAGGAGGAGG 674
 DB 489 GAGCGACAGAAATATACAGCGGAGCTATGAGCGCTTACAGAAACATCCGCGAGGAGGAGG 548
 QY 675 AGTCAGGGGCTGTGAAAGAACTTTGCCCAACATCATGAGGAGGAGGAGGAGGAGGAGG 734

DB 549 AGTCAGGGGCTGTGAAAGAACTTTGCCCAACATCATGAGGAGGAGGAGGAGGAGGAGG 608
 QY 735 TGTGAAGTTCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 794
 DB 609 TGTGAAGTTCCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 668
 QY 795 TGAACAATTCCTGCGACCTTTGTCTGTGCTTGGAGGCGGCTTCTGTGCGACAGTGT 854
 DB 669 TGAACAATTCCTGCGACCTTTGTCTGTGCTTGGAGGCGGCTTCTGTGCGACAGTGT 728
 QY 855 GGCCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 914
 DB 729 GGCCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 788
 QY 915 CAGCCCCCTGACATGATATGAAGATGTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 974
 DB 789 CAGCCCCCTGACATGATATGAAGATGTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 848
 QY 975 GGGATTTACACCTCCTTTTGTGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1034
 DB 849 GGGATTTACACCTCCTTTTGTGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 908
 QY 1035 TGAAGAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1094
 DB 909 TGAAGAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 968
 QY 1095 AAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1148
 DB 969 AAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1022

RESULT 11

AAV72691
 ID AAV72691 standard; cDNA; 1132 BP.

AC AAV72691;

DT 22-FEB-1999 (first entry)

XX DE Human uncoupling protein UCP3s encoding cDNA.

XX KW Human, uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;
 XX KW adenine triphosphate; mitochondria; skeletal muscle; gene therapy;
 XX KW thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;
 XX KW insulin sensitivity; neuromuscular disease; ss.

OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT CDS 154..991
 XX FT /*tag= a
 XX FT /product= "UCP3s"

PN W09850542-A1.

PD 12-NOV-1998.

PF 05-MAY-1998; 98MO-EP002645.

PR 07-MAY-1997; 97CH-00001072.

PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Giacobino J, Muzzin P, Boss O;

DR WPI: 1998-610382/51.

DR P-PSDB; AAM83380.

XX PT New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful
 XX PT for controlling thermogenesis in human skeletal muscle and heart, e.g.
 XX PT for treating obesity and cachexia.

XX Claim 3, Page 17-18, 26pp; English.

PS The present sequence encodes human uncoupling protein UCP3. UCP3
 CC uncouples oxidative phosphorylation and synthesis of adenosine
 CC triphosphate in the mitochondria of skeletal muscle. The coding sequences
 CC for UCP3L and UCP3S are useful for gene therapy of dysfunctions of
 CC thermogenesis in human skeletal muscle and heart which result from a lack
 CC of UCP3 and which can induce disorders such as obesity or cachexia.
 CC Antisense oligonucleotides to UCP3L and UCP3S can be used for correcting
 CC an excess of UCP3. Modification of endogenous UCP3 activity (using
 CC activators or inhibitors of UCP3) is used to induce bodyweight loss (loss
 CC of adipose mass and maintenance of the lean mass) in all types of obesity
 CC by promoting the dissipation of energy; for preventing an excessive
 CC weight regain following restrictive food diet or after ceasing a physical
 CC training programme; for preventing and treating type II diabetes by
 CC increasing sensitivity to insulin; for preventing hypertension; for
 CC improving muscle mass in states of cachexia; for treatment of
 CC insufficiencies or disturbances of cardiac rhythm due to a dysfunction of
 CC UCP3; and for the treatment of neuromuscular diseases due to a
 CC dysfunction of UCP3. The uncoupling proteins can also be used to raise
 CC antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows
 CC generation of transgenic animals, e.g. for screening substances which
 CC modify UCP3 expression or activity or for investigating the biological
 CC role of UCP3

XX Sequence 1132 BP, 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match 79.7%; Score 981.4; DB 2; Length 1132;
 Best Local Similarity 99.4%; Pred. No. 2.7e-233;
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCTTGGGATGAGGCGCTTAGGAGGCGGCTGTGCGCCCGGCGGAGGACTCAAGGC 60
 DB 1 TCTTGGGATGAGGCGCTTAGGAGGCGGCTGTGCGCCCGGCGGAGGACTCAAGGC 60
 QY 61 CCAGCGCTGCACTGAGAGCCAGGCGTGTGAGACAGGCTCTCTCTCTCTCTCTCTCT 120
 DB 61 CCAGCGCTGCACTGAGAGCCAGGCGTGTGAGACAGGCTCTCTCTCTCTCTCTCTCT 120
 QY 121 CCTTAAAGGAGCTGAGGAGGCTTTCAGAGCTATGTGAGTCTGAGTCTGAGTCTGAG 180
 DB 121 CCTTAAAGGAGCTGAGGAGGCTTTCAGAGCTATGTGAGTCTGAGTCTGAGTCTGAG 180
 QY 181 CCTTAAAGGAGCTGAGGAGGCTTTCAGAGCTATGTGAGTCTGAGTCTGAGTCTGAG 240
 DB 181 CCTTAAAGGAGCTGAGGAGGCTTTCAGAGCTATGTGAGTCTGAGTCTGAGTCTGAG 240
 QY 241 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 300
 DB 241 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 300
 QY 301 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 360
 DB 301 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 360
 QY 361 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 420
 DB 361 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 420
 QY 421 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
 DB 421 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
 QY 481 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 540
 DB 481 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 540
 QY 541 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 600
 DB 541 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 600
 QY 601 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660
 DB 601 GTTACCTTTCAGACTGAGACAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660

DB 601 CTCGGGCGCATCCAGAGGAGCAGAAATATACGCGGAGCTATGAGCGCTTACAGAACCATC 660
 QY 661 GCGAGGAGGAGAGAGTCCAGGCGGCTGTGAGAAAGAACTTGTCCCAATCATGAGAGAT 720
 DB 661 GCGAGGAGGAGAGAGTCCAGGCGGCTGTGAGAAAGAACTTGTCCCAATCATGAGAGAT 720
 QY 721 GCTATCGTCACTGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 780
 DB 721 GCTATCGTCACTGATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 780
 QY 781 TACCACTGCTCACTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 840
 DB 781 TACCACTGCTCACTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 840
 QY 841 TGTGCAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 900
 DB 841 TGTGCAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 900
 QY 901 CCAGGCGAGTACTTCCAGGCGGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 960
 DB 901 CCAGGCGAGTACTTCCAGGCGGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 960
 QY 961 ACAGCTTCTCAAGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 991
 DB 961 ACAGCTTCTCAAGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 991

RESULT 12

AAZ29324
 ID AAZ29324 standard; cDNA, 1132 BP.

AAZ29324;
 29-FEB-2000 (first entry)

Human uncoupling protein-3S cDNA.

Human uncoupling protein-3S; UCP; immune response; electron transport;
 oxidative phosphorylation; Major histocompatibility complex;
 MHC class II HLA-DR; proton motor force; mitochondrial membrane potential;
 mitochondrial metabolism; cancer; autoimmune disease;
 neurodegenerative disorder; de.

Homo sapiens.

Key Location/Qualifiers

CDS /tag= a
 /product= "Human uncoupling protein-3S"

MO9953953-A2.

28-OCT-1999.

30-MAR-1999; 99WO-US006874.

17-APR-1998; 98US-0082250P.

29-JUL-1998; 98US-0094519P.

24-SEP-1998; 98US-0101580P.

(UYVE-) UNIV VERMONT.

Newell MK;

WPI, 2000-096773/08.

F-PSDB; AAY44293.

Use of cell surface and membrane characteristics for developing products
 for treating cancers, autoimmune diseases or neurodegenerative diseases.
 Disclosure, Page 119-120; 123pp; English.

CC The present sequence encodes human uncoupling protein-3s. UCPS can cause
 CC the reversible uncoupling of electron transport and oxidative
 CC phosphorylation, which leads to a decrease in the mitochondrial membrane
 CC potential. This can induce lysis in a tumour cell by inducing the
 CC expression of MHC class II-HLA-DR. These methods can be used for
 CC regulating cell growth and division to control disease processes by
 CC manipulating mitochondrial metabolism and the expression of cell surface
 CC immune proteins. They can be used for treating diseases associated with
 CC excessive cellular division, aberrant differentiation, and premature
 CC cellular death, e.g. cancers, autoimmune diseases, neurodegenerative
 CC disorders etc

XX Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match 79.7%; Score 981.4; DB 3; Length 1132;
 Best Local Similarity 99.4%; Pred. No. 2.7e-233;
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 TCCTGGAGTGGAGCCCTAGAGGCGCTGTGCTGCTCCCTGCGGAGGAGGACTCAGAGCC 60
 1 TCCTGGAGTGGAGCCCTAGAGGCGCTGTGCTGCTCCCTGCGGAGGAGGACTCAGAGCC 60
 61 CCACCGCTGCTGAGAGCCAGGAGGCTGTGAGAGGCTCTCTCTGGAACCTCTCTCG 120
 61 CCACCGCTGCTGAGAGCCAGGAGGCTGTGAGAGGCTCTCTCTGGAACCTCTCTCG 120
 121 CCCTAAAGGAGTGGGAGAGCTTCCAGAGCTATGAGTGTGAGTGAAGCTTGAAGCTG 180
 121 CCCTAAAGGAGTGGGAGAGCTTCCAGAGCTATGAGTGTGAGTGAAGCTTGAAGCTG 180
 181 CCTCCACCATGCTGTGAGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 181 CCTCCACCATGCTGTGAGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 241 GTTACCTTTCATGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 241 GTTACCTTTCATGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 301 GTTCAGAGCGGCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360
 301 GTTCAGAGCGGCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360
 361 CGGAGTGAAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 361 CGGAGTGAAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 421 AGCTTGCGCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 421 AGCTTGCGCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
 481 GGGCGGAGCAACTCCAGGCTCTACTACCCGAGATTTGGCGGCTGTGAGCAGCAGAGCCATG 540
 481 GGGCGGAGCAACTCCAGGCTCTACTACCCGAGATTTGGCGGCTGTGAGCAGCAGAGCCATG 540
 541 GCGGTGACCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 541 GCGGTGACCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 601 CTGGGCGCATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 601 CTGGGCGCATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 661 GCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 661 GCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 721 GGTATGCTCAACTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 780
 721 GGTATGCTCAACTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 780
 781 TACCACTGCTCACTGACCACTTCCCTGCACTTTGTCTGTGCTTTGAGAGCGGCTTC 840
 781 TACCACTGCTCACTGACCACTTCCCTGCACTTTGTCTGTGCTTTGAGAGCGGCTTC 840

QY 841 TGTGCGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 DB 841 TGTGCGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 QY 901 CCAGGCGCATCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
 DB 901 CCAGGCGCATCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
 QY 961 ACAGCTTCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 991
 DB 961 ACAGCTTCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 991

RESULT 13
 AAS14820
 ID AAS14820 standard; cDNA; 1132 BP.

AC AAS14820;
 XX
 DT 13-DEC-2001 (first entry)

DE Human cDNA encoding partial UCP-3s protein.

KW Human; Uncoupling protein; UCP-3s; ss; transgenic plant; fuel metabolism;
 KW antibacterial; bacterial infection; environmental stress; food.

OS Homo sapiens.

FT Key Location/Qualifiers
 FT CDS 127..981
 FT /*tag= a
 FT /product= "UCP-3s"
 FT /partial
 FT /note= "No start codon"

PN MO200175131-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US010236.

PR 31-MAR-2000; 2000US-0193533P.

PA (UYTR-) UNIV TECHNOLOGY CORP.

PI Berry-Lowe SL, Newell MK;

DR WPI: 2001-626442/72.

PT P-PSDB; AAU09078.

PS Plants expressing heterologous cell-wall uncoupling protein, have altered
 metabolism, resistance to infection and stress sensitivity.

PS Disclosure; Page 60-61; 72pp; English.

CC The invention relates to a transgenic plant expressing a cell-wall UCP
 CC (uncoupling protein) encoded by a heterologous gene. The heterologous
 CC UCP, when expressed in the plant cell wall, plasma membrane or
 CC chloroplast regulates the fuel metabolism of the plant. Regulating
 CC expression or activity of UCP is used to control fuel metabolism,
 CC especially reducing UCP expression produces nutritionally improved plants
 CC and protects against infection e.g. bacterial, while decreasing
 CC expression improves sensitivity to light and cold. Altering UCP activity
 CC can improve crop productivity and durability towards environmental
 CC stress, and it eliminates time-consuming and expensive maintenance and
 CC repeated application of chemicals. The present sequence encodes human UCP
 CC -3s and is used as the heterologous UCP in the method of the invention

XX Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;

Query Match 79.7%; Score 981.4; DB 5; Length 1132;
 Best Local Similarity 99.4%; Pred. No. 2.7e-233;

| Matches | 985; Conservative | 0; Mismatches | 6; Indels | 0; Gaps | 0; |
|---------|-------------------|---|-----------|---------|----|
| QY | 1 | TCCTGGAGTGAAGCCCTTAAGAGAGCCCTGTGCTGCTCCCTGCGGTGGCAGACTCAAGCC | 60 | | |
| DB | 1 | TCCTGGAGTGAAGCCCTTAAGAGAGCCCTGTGCTGCTCCCTGCGGTGGCAGACTCAAGCC | 60 | | |
| QY | 61 | CCACCGGCGCACTGAAGCCCGAGGCGTGTGGAGCAGCCCTCTCCCTTGGACCTCCCTCGG | 120 | | |
| DB | 61 | CCACCGGCGCACTGAAGCCCGAGGCGTGTGGAGCAGCCCTCTCCCTTGGACCTCCCTCGG | 120 | | |
| QY | 121 | CCCTAAAGGAGCTGGGCGAGAGCCCTTCAAGACTATGTTGGACTGAAGCCTTTCAGAGCTG | 180 | | |
| DB | 121 | CCCTAAAGGAGCTGGGCGAGAGCCCTTCAAGACTATGTTGGACTGAAGCCTTTCAGAGCTG | 180 | | |
| QY | 181 | CTCTCCACCATGCTGTGAAGTTCTGTGGGCGAGGCGACAGCAAGCAAGCTGTTTGTGACCTC | 240 | | |
| DB | 181 | CTCTCCACCATGCTGTGAAGTTCTGTGGGCGAGGCGACAGCAAGCAAGCTGTTTGTGACCTC | 240 | | |
| QY | 241 | GTTACCTTTCACTGAGAGACAGAGCCCAAGGTCGCGCTGCAAGATCCAGGGGAGAAACAGGCG | 300 | | |
| DB | 241 | GTTACCTTTCACTGAGAGACAGAGCCCAAGGTCGCGCTGCAAGATCCAGGGGAGAAACAGGCG | 300 | | |
| QY | 301 | GTCAGAGCGCCCGGCTGTGACAGTACCGTGGCGGTGTGGGCAACCATCTGACATGCTG | 360 | | |
| DB | 301 | GTCAGAGCGCCCGGCTGTGACAGTACCGTGGCGGTGTGGGCAACCATCTGACATGCTG | 360 | | |
| QY | 361 | CGGACTGAGGGTCCCTGAGAGCCCTTAAGATGGGCTGTGGCGGCTGCAAGGCGCAGATG | 420 | | |
| DB | 361 | CGGACTGAGGGTCCCTGAGAGCCCTTAAGATGGGCTGTGGCGGCTGCAAGGCGCAGATG | 420 | | |
| QY | 421 | AGCTTGCTCTCATTCGCGATCGGCTCTATGACTCCCTCAAGAGGTATGACACCCCAAA | 480 | | |
| DB | 421 | AGCTTGCTCTCATTCGCGATCGGCTCTATGACTCCCTCAAGAGGTATGACACCCCAAA | 480 | | |
| QY | 481 | GCGCGGAGCAACTCCAGGCTCACTACCGGATTTTGGCGGCTGACCAAGAGCCATG | 540 | | |
| DB | 481 | GCGCGGAGCAACTCCAGGCTCACTACCGGATTTTGGCGGCTGACCAAGAGCCATG | 540 | | |
| QY | 541 | GCGGTAACCTGTGCTGAGAGCCCAAGATGTGTGAAGTTCGATTTCAAGGCGCATACAC | 600 | | |
| DB | 541 | GCGGTAACCTGTGCTGAGAGCCCAAGATGTGTGAAGTTCGATTTCAAGGCGCATACAC | 600 | | |
| QY | 601 | CTCGGCGCACTCAGAGGAGCAGAAATACAGGCGGATCTATGAGAGCCCTACAGAACCATC | 660 | | |
| DB | 601 | CTCGGCGCACTCAGAGGAGCAGAAATACAGGCGGATCTATGAGAGCCCTACAGAACCATC | 660 | | |
| QY | 661 | GCCAGGAGGAGAGGTGAGAGGCGCTGTGGAAAGAACTTGGCCCAACATCATGAGGAT | 720 | | |
| DB | 661 | GCCAGGAGGAGAGGTGAGAGGCGCTGTGGAAAGAACTTGGCCCAACATCATGAGGAT | 720 | | |
| QY | 721 | GCTATGCTCACTGTGCTGAGGTGTGACTTACGACATCTCTCAGAGAGAGCTGTGAC | 780 | | |
| DB | 721 | GCTATGCTCACTGTGCTGAGGTGTGACTTACGACATCTCTCAGAGAGAGCTGTGAC | 780 | | |
| QY | 781 | TACCACTGCTCACTGACAACTTCCCTGCGCACTTGTCTCTGCTTTGGAGCCGAGCTTC | 840 | | |
| DB | 781 | TACCACTGCTCACTGACAACTTCCCTGCGCACTTGTCTCTGCTTTGGAGCCGAGCTTC | 840 | | |
| QY | 841 | TGTGCAAGTGTGCTGCTGAGGCTGAGAGAGGATGAGAGCCGGATATGAACTCACT | 900 | | |
| DB | 841 | TGTGCAAGTGTGCTGCTGAGGCTGAGAGAGGATGAGAGCCGGATATGAACTCACT | 900 | | |
| QY | 901 | CCAGGCGAGTACTTCAAGCCCTCTGCACTGTATGATTAAGATGTGGCCAGAGAGGCCCC | 960 | | |
| DB | 901 | CCAGGCGAGTACTTCAAGCCCTCTGCACTGTATGATTAAGATGTGGCCAGAGAGGCCCC | 960 | | |
| QY | 961 | ACAGCTTCTTACAGAGGGGTGAGCTCTCTCT | 991 | | |
| DB | 961 | ACAGCTTCTTACAGAGGGGTGAGCTCTCTCTCT | 991 | | |

RESULT 14
AAD02389

| | | | | |
|-----------------------|---|--|--------------------------------|--|
| ID | AAD02389 standard; cDNA; 1132 BP. | | | |
| XX | | | | |
| AC | AAD02389; | | | |
| DT | 24-APR-2001 (first entry) | | | |
| XX | | | | |
| DE | Human uncoupling protein, UCP-3S cDNA. | | | |
| XX | | | | |
| KM | Human; uncoupling protein; UCP-3S; cancer; brain; renal; antiviral; | | | |
| KM | antibacterial; antifungal; cytostatic; immunosuppressive; scleroderma; | | | |
| KM | antiarthritic; dermatological; UCP inhibitor; therapy; antiheumatic; | | | |
| KM | rheumatoid arthritis; leukaemia; tumour; autoimmune disease; SLE; | | | |
| KM | systemic lupus erythematosus; celiac disease; infectious disease; | | | |
| KM | pemphigus vulgaris; ss. | | | |
| OS | Homo sapiens. | | | |
| XX | | | | |
| FH | Key | | | |
| FT | CDS | | | |
| FT | Location/Qualifiers | | | |
| FT | 154..981 | | | |
| FT | /*tag= a | | | |
| FT | /product= "Human UCP-3S protein" | | | |
| XX | | | | |
| PN | WO200078941-A2. | | | |
| XX | | | | |
| PD | 28-DEC-2000. | | | |
| XX | | | | |
| PF | 22-JUN-2000; 2000WO-US017245. | | | |
| XX | | | | |
| PR | 23-JUN-1999; 99US-0140574P. | | | |
| XX | | | | |
| PA | (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE. | | | |
| XX | | | | |
| PI | Newell MK; | | | |
| XX | | | | |
| DR | WPI; 2001-102716/11. | | | |
| XX | | | | |
| DR | P-PSDB; AAY72343. | | | |
| XX | | | | |
| PT | Inhibiting plasma membrane uncoupling protein expression in tumor cells | | | |
| PT | and rapidly dividing bacterial cells, for treating cancer and infectious | | | |
| PT | diseases. | | | |
| XX | | | | |
| PS | Disclosure; Page 105-106; 106pp; English. | | | |
| XX | | | | |
| CC | The present sequence is a cDNA encoding human Uncoupling Protein, UCP-3S. | | | |
| CC | The present invention relates to a method for inhibiting the expression | | | |
| CC | of plasma membrane uncoupling protein (UCP) in a cell by a plasma | | | |
| CC | membrane UCP inhibitor. UCP is expressed on lysosomal membranes and | | | |
| CC | plasma membranes of rapidly dividing cells, but absent in growth arrested | | | |
| CC | or chemotherapy resistant cells. This method is useful in the inhibition | | | |
| CC | of plasma membrane UCP expression in tumor cells, lymphocytes, | | | |
| CC | pancreatic beta cells, rapidly dividing bacterial cells or B cells. UCP | | | |
| CC | inhibitor is useful in the prevention and treatment of infectious | | | |
| CC | disease, rheumatoid arthritis, scleroderma and cancers such as brain | | | |
| CC | cancer, leukemia, renal cancer, and tumours. The UCP activator is useful | | | |
| CC | in the treatment of autoimmune diseases such as systemic lupus | | | |
| CC | erythematosus (SLE), celiac disease and pemphigus vulgaris. UCP is also | | | |
| CC | useful for inducing cellular division in nerve cells | | | |
| XX | | | | |
| SQ | Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other; | | | |
| XX | | | | |
| Query Match | 79.7%; | Score 981.4; | DB 5; Length 1132; | |
| Beat Local Similarity | 99.4%; | Pred. No. 2.7e-233; | | |
| Matches | 985; | Conservative 0; | Mismatches 6; Indels 0; Gaps 0 | |
| QY | 1 | TCCTGGAGTGAAGCCCTTAAGAGAGCCCTGTGCTGCTCCCTGCGGTGGCAGACTCAAGCC | 60 | |
| DB | 1 | TCCTGGAGTGAAGCCCTTAAGAGAGCCCTGTGCTGCTCCCTGCGGTGGCAGACTCAAGCC | 60 | |
| QY | 61 | CCACCGGCGCACTGAAGCCCGAGGCGTGTGGAGCAGCCCTCTCCCTTGGACCTCCCTCGG | 120 | |
| DB | 61 | CCACCGGCGCACTGAAGCCCGAGGCGTGTGGAGCAGCCCTCTCCCTTGGACCTCCCTCGG | 120 | |
| QY | 121 | CCCTAAAGGAGCTGGGCGAGAGCCCTTCAAGACTATGTTGGACTGAAGCCTTCAAGACTG | 180 | |

Db 121 CCTTAAAGGAGCTTGGGAGAGGCTTCCAGACTATGTTGGACTGAAGCTTCAAGACGTG 180
 Qy 181 CTTCCACCATGAGCTGTGTAAGTTCTGGGGGAGGACAGACGCTGTTTCTGAAGCTC 240
 Db 181 CTTCCACCATGAGCTGTGTAAGTTCTGGGGGAGGACAGACGCTGTTTCTGAAGCTC 240
 Qy 241 GTTACTCTTCCATGAGACACAGCCAGAGTCCGCTGTCACATATCCAGGGGAGAAACCGGGG 300
 Db 241 GTTACTCTTCCATGAGACACAGCCAGAGTCCGCTGTCACATATCCAGGGGAGAAACCGGGG 300
 Qy 301 GTTCAAGAGGCGCGGCTGTGAGTACCGTGGGCTGTGGGACCATCTCTGACATGATG 360
 Db 301 GTTCAAGAGGCGCGGCTGTGAGTACCGTGGGCTGTGGGACCATCTCTGACATGATG 360
 Qy 361 CGGACTGAGGAGTCCCTGACAGCCCTTCAATGAGGCTGTGGCGGCTGACAGCCAGATG 420
 Db 361 CGGACTGAGGAGTCCCTGACAGCCCTTCAATGAGGCTGTGGCGGCTGACAGCCAGATG 420
 Qy 421 AGCTTGGCTCCATCGGACTGGCTCTATGACTCCGTCAAGAGGTTGACACCCCAAA 480
 Db 421 AGCTTGGCTCCATCGGACTGGCTCTATGACTCCGTCAAGAGGTTGACACCCCAAA 480
 Qy 481 GGGGGGAGCACTCCAGCCTCACTACCCGGAATTTGGCGGCTGACACAGAGGCTATG 540
 Db 481 GGGGGGAGCACTCCAGCCTCACTACCCGGAATTTGGCGGCTGACACAGAGGCTATG 540
 Qy 541 GGGGTGACCTGTGCGCCAGCCACAGATGTGTGAGAGTCCGATTTGAGGCGACATACAC 600
 Db 541 GGGGTGACCTGTGCGCCAGCCACAGATGTGTGAGAGTCCGATTTGAGGCGACATACAC 600
 Qy 601 CTGGGGCCATCCAGAGGACACAGAAATACAGCGGACATATGACCCCTACAGAACCATC 660
 Db 601 CTGGGGCCATCCAGAGGACACAGAAATACAGCGGACATATGACCCCTACAGAACCATC 660
 Qy 661 GCGAGGAGGAGGAGTCAAGGGGCTGTGAGAAAGAACTTGGCCCAACATCATAGAAAT 720
 Db 661 GCGAGGAGGAGGAGTCAAGGGGCTGTGAGAAAGAACTTGGCCCAACATCATAGAAAT 720
 Qy 721 GGTATGTCACACTGTGTCTGAGTGTGACCTTACAGATCCTCAAGAGAGAGCTGTGAG 780
 Db 721 GGTATGTCACACTGTGTCTGAGTGTGACCTTACAGATCCTCAAGAGAGAGCTGTGAG 780
 Qy 781 TACCACTGTCTCACTACAACTTCCCTGCGCACTTGTCTGTGCTTTGAGAGCCGCTTC 840
 Db 781 TACCACTGTCTCACTACAACTTCCCTGCGCACTTGTGTCTGTGCTTTGAGAGCCGCTTC 840
 Qy 841 TGTGCGACAGTGTGCTCTCCCGGTGAGAGTGTGTAAGACCCGATATGAACTACCT 900
 Db 841 TGTGCGACAGTGTGCTCTCCCGGTGAGAGTGTGTAAGACCCGATATGAACTACCT 900
 Qy 901 CCAGGCGAGTACTTCAAGCCCTCGACTGTATGATTAAGATGTTGGCCCAAGAGGCCCC 960
 Db 901 CCAGGCGAGTACTTCAAGCCCTCGACTGTATGATTAAGATGTTGGCCCAAGAGGCCCC 960
 Qy 961 ACAGCCTTCTTACAGAGGATTTACACCTCT 991
 Db 961 ACAGCCTTCTTACAGAGGATTTACACCTCTCT 991
 RESULT 15
 ABQ73000
 ID ABQ73000 standard; cDNA, 1132 BP.
 AC
 XX ABQ73000;
 XX
 DT 20-SEP-2002 (first entry)
 XX
 DE UCP35 cDNA clone nucleotide sequence.
 XX
 KM UCP31; UCP35; diabetes; obesity; diabetic related condition; GKR; gene therapy; anti-diabetic; anorectic; cardiomy; nephrotropic; Gk; antilipemic; blood glucose; glucokinase regulatory protein; liver;

KW glucokinase; hepatic triglyceride accumulation; fibrinogen; HDL; KW
 KW hepatic fatty acid oxidation; high density lipoprotein; cholesterol; KW
 KW glucose; gestational diabetes; hyperglycemic related disorder; KW
 OS kidney related disorder; cardiovascular disorder; gene; se.
 XX
 XX
 FH Unidentified.
 FT
 FT Key Location/Qualifiers
 CDS 154..981
 FT /*tag= a
 FT /product= "UCP35 protein"
 PN
 XX US2002065239-A1.
 PD 30-MAY-2002.
 XX
 XX 14-MAR-2001; 2001US-00808457.
 PF 15-MAR-2000; 2000US-0266328P.
 PR
 XX
 XX (CAPL/) CAPLAN S L.
 PA (BOET/) BOETTCHER B R.
 PA (SLOS/) SLOSBERG B D.
 PA (CONN/) CONNELLY S.
 PA (KALE/) KALEKO M.
 PA (DESA/) DESAI U J.
 XX
 XX Caplan SL, Boettcher BR, Slosberg BD, Connelly S, Kaleko M,
 PI Desai UJ;
 DR WPI: 2002-556735/59.
 DR P-PSDB; ABB81611.
 XX
 XX Treating condition related to elevated blood glucose levels, especially
 PT diabetes or obesity, involves administering polynucleotide sequence
 PT encoding glucokinase regulatory protein, to a subject.
 PS
 XX Disclosure; Page 17-18; 42pp; English.
 XX
 XX The present invention describes a method (M1) for treating a condition
 CC related to elevated blood glucose levels, which involves administering a
 CC polynucleotide sequence encoding a glucokinase regulatory protein (GKR),
 CC to a subject. Also described: (1) increasing liver glucokinase (GK)
 CC activity, by administering a polynucleotide sequence encoding GKR; and
 CC (2) a method (M2) treating diabetes or diabetes-related condition, by
 CC administering to a subject, one or more metabolism modifying proteins and
 CC peptides in combination with GK or GKR, or their combination. (M1) and
 CC (M2) can be used for treating diabetes (type I and II diabetes) or
 CC diabetes-related conditions such as obesity, increased hepatic
 CC triglyceride accumulation, reduced hepatic fatty acid oxidation,
 CC increased fibrinogen levels, decreased apo A-I levels, decreased high
 CC density lipoprotein (HDL) cholesterol levels and decreased hepatic
 CC glucose utilization. The methods are also useful for treating gestational
 CC diabetes, hyperglycemic related disorders such as increased cholesterol,
 CC kidney related disorders and cardiovascular disorders. The methods
 CC overcome a limitation to the over-expression of GK in the liver which
 CC usually increases liver size and hepatic fat accumulation in normal and
 CC diabetic mice. The present sequence encodes a UCP35 protein which is
 CC given in the exemplification of the present invention
 XX
 SQ Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T; 0 U; 0 Other;
 Query Match 79.7%; Score 981.4; DB 6; Length 1132;
 Best Local Similarity 99.4%; Pred. No. 2.7e-233;
 Matches 985; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 TCTGGAGTGAAGCCCTAGAGAGCCCTGTGTGCTCCCTGCGGTGAGAGTCAAGCC 60
 Db 1 TCTGGAGTGAAGCCCTAGAGAGCCCTGTGTGCTCCCTGCGGTGAGAGTCAAGCC 60
 Qy 61 CCACGCTGCTCACTGAAGCCCAAGGCTGTGAGACAGCTTCTCTTGAAGCTTCTCGG 120
 Db 61 CCACGCTGCTCACTGAAGCCCAAGGCTGTGAGACAGCTTCTCTTGAAGCTTCTCGG 120

QY 121 CCTAAAGGAGCTGGGAGAGAGCTTCCAGACTATGTTGACTGAGACCTTCAGACGTG 180
DB 121 CCTAAAGGAGCTGGGAGAGAGCTTCCAGACTATGTTGACTGAGACCTTCAGACGTG 180
QY 181 CCTCCACCAATGGCTGTGAAGTTCTTGGGGGAGGCAAGAGCTGTTTGTGACTTC 240
DB 181 CCTCCACCAATGGCTGTGAAGTTCTTGGGGGAGGCAAGAGCTGTTTGTGACTTC 240
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QY 301 GTCCAGACGCGCCGCTGTCAGTACCGTGGCGTGGTGGGCAACCATCTGACATGGTG 360
DB 301 GTCCAGACGCGCCGCTGTCAGTACCGTGGCGTGGTGGGCAACCATCTGACATGGTG 360
QY 361 CGGACTGAGGGTCCCTGCAAGCCCTTAACAATGGGCTGGTGGCCGCTGCAAGCCAGATG 420
DB 361 CGGACTGAGGGTCCCTGCAAGCCCTTAACAATGGGCTGGTGGCCGCTGCAAGCCAGATG 420
QY 421 AGCTTCGCTCCATCGAGCTGAGTACCGGCTTAATGACTCCGCAAGAGTGAACCCCAAA 480
DB 421 AGCTTCGCTCCATCGAGCTGAGTACCGGCTTAATGACTCCGCAAGAGTGAACCCCAAA 480
QY 481 GCGCGGACAACTCCAGCTCACTAACCGGATTTTGGCGGCTGCAACAAGAGCCATG 540
DB 481 GCGCGGACAACTCCAGCTCACTAACCGGATTTTGGCGGCTGCAACAAGAGCCATG 540
QY 541 GCGGTGACTTGTGCCCAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGCATAC 600
DB 541 GCGGTGACTTGTGCCCAGCCCAAGATGTGTGAAGTCCGATTTCAAGCCAGCATAC 600
QY 601 CTCGGGCAATCCAGGAGCAGAAATACAGCGGACTATGAGCGCTTACAGAACATC 660
DB 601 CTCGGGCAATCCAGGAGCAGAAATACAGCGGACTATGAGCGCTTACAGAACATC 660
QY 661 GCCAGGAGGAGAGAGTCAAGGGGCTGTGGAAGAACTTTGCCCAACATCATGAGGAT 720
DB 661 GCCAGGAGGAGAGAGTCAAGGGGCTGTGGAAGAACTTTGCCCAACATCATGAGGAT 720
QY 721 GCTATGTCAACTGTGTGAGGTGTGACTTACGACATCTTCAAGGAGAGCTGTGAC 780
DB 721 GCTATGTCAACTGTGTGAGGTGTGACTTACGACATCTTCAAGGAGAGCTGTGAC 780
QY 781 TACCACTGCTCACTGACAACTTCCCTGCGCACTTGTCTGCTTGGAGCGGCTTC 840
DB 781 TACCACTGCTCACTGACAACTTCCCTGCGCACTTGTCTGCTTGGAGCGGCTTC 840
QY 841 TGTGCCACAGTGTGCTCCCGGTGAGAGTGTGAAGCCGATATGAATCACT 900
DB 841 TGTGCCACAGTGTGCTCCCGGTGAGAGTGTGAAGCCGATATGAATCACT 900
QY 901 CCAAGGCACTTCAAGCCCTTCACTGTATGATAAAGATGTGGCCCAAGAGGCGCC 960
DB 901 CCAAGGCACTTCAAGCCCTTCACTGTATGATAAAGATGTGGCCCAAGAGGCGCC 960
QY 961 ACAGCTTTTACAAAGGATTTACACCTCT 991
DB 961 ACAGCTTTTACAAAGGATTTACACCTCT 991

Search completed: May 18, 2004, 12:31:25
Job time : 532 secs

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OM protein - protein search, using SW model

Run on: May 17, 2004, 11:50:46 ; Search time 23 Seconds
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Title: US-09-423-410-4
Perfect score: 1620
Sequence: 1 MVLGKPSDVPPTMAVFLGA.....TYEQLKRALMKVQMLRESPF 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/prodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1620 | 100.0 | 312 | 3 | US-09-142-565-2 Sequence 2, Appl1 |
| 2 | 1620 | 100.0 | 312 | 4 | US-09-808-457-2 Sequence 2, Appl1 |
| 3 | 1620 | 100.0 | 312 | 4 | US-09-423-410-4 Sequence 4, Appl1 |
| 4 | 1599 | 98.7 | 310 | 4 | US-09-743-847-5 Sequence 5, Appl1 |
| 5 | 1430 | 88.3 | 275 | 4 | US-09-808-457-4 Sequence 4, Appl1 |
| 6 | 1430 | 88.3 | 275 | 4 | US-09-423-410-6 Sequence 6, Appl1 |
| 7 | 1369 | 84.5 | 308 | 2 | US-08-937-466-2 Sequence 2, Appl1 |
| 8 | 1369 | 84.5 | 308 | 2 | US-09-172-528-2 Sequence 2, Appl1 |
| 9 | 1369 | 84.5 | 308 | 3 | US-09-318-199-2 Sequence 2, Appl1 |
| 10 | 1369 | 84.5 | 308 | 3 | US-09-503-579-2 Sequence 2, Appl1 |
| 11 | 1341 | 82.8 | 432 | 2 | US-08-937-466-4 Sequence 4, Appl1 |
| 12 | 1341 | 82.8 | 432 | 2 | US-09-172-528-4 Sequence 4, Appl1 |
| 13 | 1341 | 82.8 | 432 | 3 | US-09-318-199-4 Sequence 4, Appl1 |
| 14 | 1341 | 82.8 | 432 | 3 | US-09-503-579-4 Sequence 4, Appl1 |
| 15 | 1152.5 | 71.1 | 309 | 4 | US-10-001-0518-2 Sequence 2, Appl1 |
| 16 | 1149.5 | 71.0 | 309 | 4 | US-09-743-847-4 Sequence 4, Appl1 |
| 17 | 1147.5 | 70.8 | 309 | 1 | US-08-518-8788-51 Sequence 51, Appl1 |
| 18 | 1147.5 | 70.8 | 309 | 2 | US-08-807-861A-51 Sequence 51, Appl1 |
| 19 | 1147.5 | 70.8 | 309 | 2 | US-08-470-868A-51 Sequence 51, Appl1 |
| 20 | 1147.5 | 70.8 | 309 | 3 | US-09-210-681-51 Sequence 51, Appl1 |
| 21 | 1147.5 | 70.8 | 309 | 3 | US-08-946-719A-51 Sequence 51, Appl1 |
| 22 | 1147.5 | 70.8 | 309 | 4 | US-09-547-983-51 Sequence 51, Appl1 |
| 23 | 1110.5 | 68.5 | 299 | 2 | US-08-518-8788-56 Sequence 56, Appl1 |
| 24 | 1110.5 | 68.5 | 299 | 2 | US-08-470-868A-56 Sequence 56, Appl1 |
| 25 | 1098 | 67.8 | 256 | 2 | US-08-937-466-6 Sequence 6, Appl1 |
| 26 | 1098 | 67.8 | 256 | 2 | US-09-172-528-6 Sequence 6, Appl1 |
| 27 | 1098 | 67.8 | 256 | 3 | US-09-318-199-6 Sequence 6, Appl1 |

| | | | | | |
|----|--------|------|-----|---|--------------------------------------|
| 28 | 1098 | 67.8 | 256 | 3 | US-09-503-579-6 Sequence 6, Appl1 |
| 29 | 1012.5 | 62.5 | 303 | 1 | US-08-294-522B-36 Sequence 36, Appl1 |
| 30 | 1009.5 | 62.3 | 303 | 1 | US-08-518-878B-37 Sequence 37, Appl1 |
| 31 | 1009.5 | 62.3 | 303 | 2 | US-08-807-861A-37 Sequence 37, Appl1 |
| 32 | 1009.5 | 62.3 | 303 | 2 | US-08-470-868A-37 Sequence 37, Appl1 |
| 33 | 1009.5 | 62.3 | 303 | 3 | US-09-210-681-37 Sequence 37, Appl1 |
| 34 | 1009.5 | 62.3 | 303 | 3 | US-08-946-719A-37 Sequence 37, Appl1 |
| 35 | 1009.5 | 62.3 | 303 | 4 | US-09-547-983-37 Sequence 37, Appl1 |
| 36 | 910.5 | 56.2 | 307 | 4 | US-09-743-847-3 Sequence 3, Appl1 |
| 37 | 889.5 | 54.9 | 307 | 2 | US-08-807-861A-56 Sequence 56, Appl1 |
| 38 | 889.5 | 54.9 | 307 | 3 | US-09-210-681-56 Sequence 56, Appl1 |
| 39 | 889.5 | 54.9 | 307 | 3 | US-08-946-719A-56 Sequence 56, Appl1 |
| 40 | 889.5 | 54.9 | 307 | 4 | US-09-547-983-56 Sequence 56, Appl1 |
| 41 | 887 | 54.8 | 306 | 5 | PCT-US94-09799-1 Sequence 1, Appl1 |
| 42 | 512 | 31.6 | 290 | 4 | US-09-743-847-2 Sequence 118, Appl1 |
| 43 | 512 | 31.6 | 291 | 4 | US-09-482-273-118 Sequence 2, Appl1 |
| 44 | 509.5 | 31.5 | 291 | 4 | US-09-501-558-2 Sequence 2, Appl1 |
| 45 | 485 | 29.9 | 95 | 3 | US-09-142-565-6 Sequence 6, Appl1 |

ALIGNMENTS

RESULT 1
US-09-142-565-2
Sequence 2, Application US/09142565A

Patent No. 6187560
GENERAL INFORMATION:

APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine

TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002

CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30

EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05

EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18

EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2
LENGTH: 312

TYPE: PRT
ORGANISM: HOMO SAPIEN

US-09-142-565-2

Query Match 100.0%; Score 1620; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.1e-179;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
|----|-----|---|
| QY | 1 | MVLGKPSDVPPTMAVFLGAGTACFADLVTFPLDTAKVRLQIQGENQAVQTARLVQYRG 60 |
| DB | 1 | MVLGKPSDVPPTMAVFLGAGTACFADLVTFPLDTAKVRLQIQGENQAVQTARLVQYRG 60 |
| QY | 61 | VLTGTTLMVTEBPCSPYNGLVAGLORQMSFASIRIGLVSVQVYTPKGDNSLTTRI 120 |
| DB | 61 | VLTGTTLMVTEBPCSPYNGLVAGLORQMSFASIRIGLVSVQVYTPKGDNSLTTRI 120 |
| QY | 121 | IAGCTGAMAVTCAQPDVVKVRFQASIHGPRSDRKSGETMDAVYTIAREEGVRLMK 180 |
| DB | 121 | IAGCTGAMAVTCAQPDVVKVRFQASIHGPRSDRKSGETMDAVYTIAREEGVRLMK 180 |
| QY | 181 | GLTPIINIRNAIVNCAEVYVDILKEKLDYHLTDNPFCHVSAFGAGFCATTVASPVDV 240 |
| DB | 181 | GLTPIINIRNAIVNCAEVYVDILKEKLDYHLTDNPFCHVSAFGAGFCATTVASPVDV 240 |
| QY | 241 | VKTRYNMSPGQYFSPIDCMIKVVAOEGPTAFYKGFPSFLRGSNVMVFTVEQLKRA 300 |
| DB | 241 | VKTRYNMSPGQYFSPIDCMIKVVAOEGPTAFYKGFPSFLRGSNVMVFTVEQLKRA 300 |

QY 301 LMKVQMLRESPP 312
Db 301 LMKVQMLRESPP 312

RESULT 2

US-09-808-457-2
Sequence 2, Application US/09808457
Patent No. 6608038
GENERAL INFORMATION:
APPLICANT: Boetcher, Brian
APPLICANT: Caplan, Shari
APPLICANT: Kaleko, Michael
APPLICANT: Connolly, Sheila
APPLICANT: Desai, Urv
APPLICANT: Slobberg, Eric
TITLE OF INVENTION: Methods and Compositions For Treatment
of Diabetes and Related Conditions Via Gene Therapy
FILE REFERENCE: 4-31353A/USN
CURRENT APPLICATION NUMBER: US/09/808,457
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/xxx,xxx
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Protein UCP3L
US-09-808-457-2

Query Match 100.0%; Score 1620; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.1e-179;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVOTARLVQYRG 60
Db 1 MVLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVOTARLVQYRG 60
QY 61 VLGTLITWRTGEGSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSSLTTRI 120
Db 61 VLGTLITWRTGEGSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSSLTTRI 120
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGFSRSDRKYSGTMDAYRTIAREEGVGLMK 180
Db 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGFSRSDRKYSGTMDAYRTIAREEGVGLMK 180
QY 181 GTLPNIMRNALVNCABVYTDILKEKLDYHLITDNPFCHFSAFAGCATVVASPDVY 240
Db 181 GTLPNIMRNALVNCABVYTDILKEKLDYHLITDNPFCHFSAFAGCATVVASPDVY 240
QY 241 VKTRVNSPPGQYFSPFLDCMIRKVAQEGPTAFYKGFPSFLRGSNNVMVFTYEQLKRA 300
Db 241 VKTRVNSPPGQYFSPFLDCMIRKVAQEGPTAFYKGFPSFLRGSNNVMVFTYEQLKRA 300
QY 301 LMKVQMLRESPP 312
Db 301 LMKVQMLRESPP 312

RESULT 3
US-09-423-410-4
Sequence 4, Application US/09423410
Patent No. 6620594
GENERAL INFORMATION:
APPLICANT: Giacobino, Jean-Paul
APPLICANT: Muzzin, Patrick
APPLICANT: Boss, Olivier
TITLE OF INVENTION: UNCOUPLING PROTEIN HOMOLOGUE: UCP3
FILE REFERENCE: 4-30353/A
CURRENT APPLICATION NUMBER: US/09/423,410

CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: PCT/EP98/02645
EARLIER FILING DATE: 1998-05-05
EARLIER APPLICATION NUMBER: 1072/97
EARLIER FILING DATE: 1997-05-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4

US-09-423-410-4
Sequence 5, Application US/09743847
Patent No. 6602694
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Albrandt, Keith
APPLICANT: Beaumont, Kevin
APPLICANT: Young, Andrew
TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
FILE REFERENCE: 235/108,0026
CURRENT APPLICATION NUMBER: US/09/743,847
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/092,737
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US99/15861
PRIOR FILING DATE: 1999-07-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
US-09-743-847-5

Query Match 100.0%; Score 1620; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.1e-179;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVOTARLVQYRG 60
Db 1 MVLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVOTARLVQYRG 60
QY 61 VLGTLITWRTGEGSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSSLTTRI 120
Db 61 VLGTLITWRTGEGSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKADNSSLTTRI 120
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGFSRSDRKYSGTMDAYRTIAREEGVGLMK 180
Db 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGFSRSDRKYSGTMDAYRTIAREEGVGLMK 180
QY 181 GTLPNIMRNALVNCABVYTDILKEKLDYHLITDNPFCHFSAFAGCATVVASPDVY 240
Db 181 GTLPNIMRNALVNCABVYTDILKEKLDYHLITDNPFCHFSAFAGCATVVASPDVY 240
QY 241 VKTRVNSPPGQYFSPFLDCMIRKVAQEGPTAFYKGFPSFLRGSNNVMVFTYEQLKRA 300
Db 241 VKTRVNSPPGQYFSPFLDCMIRKVAQEGPTAFYKGFPSFLRGSNNVMVFTYEQLKRA 300
QY 301 LMKVQMLRESPP 312
Db 301 LMKVQMLRESPP 312

RESULT 4

US-09-743-847-5
Sequence 5, Application US/09743847
Patent No. 6602694
GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Albrandt, Keith
APPLICANT: Beaumont, Kevin
APPLICANT: Young, Andrew
TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
FILE REFERENCE: 235/108,0026
CURRENT APPLICATION NUMBER: US/09/743,847
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/092,737
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: PCT/US99/15861
PRIOR FILING DATE: 1999-07-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
US-09-743-847-5

Query Match 98.7%; Score 1599; DB 4; Length 310;
Best Local Similarity 99.4%; Pred. No. 3.1e-177;
Matches 310; Conservative 0; Mismatches 0; Indels 2; Gaps 1;


```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-937-466-2
```

```
Query Match      84.5%; Score 1369; DB 2; Length 308;
Best Local Similarity 85.3%; Pred. No. 1,7e-150;
Matches 266; Conservative 18; Mismatches 24; Indels 4; Gaps 2;
```

```
QY 1 MVLGKPSDVPTMAVKFLGAGTAACPADLVTPPLDTAKVRLQIOGENDAVQTARLVQYRG 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MVLGKPSDVPTMAVKFLGAGTAACPADLVTPPLDTAKVRLQIOGENDAVQTARLVQYRG 57
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 VLGITILMTWRTGSPSPVNGVAGLQROMSPASIRIGLVDSVKQYTPPGADNSSLTTRI 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 58 VLGITILMTWRTGSPSPVNGVAGLQROMSPASIRIGLVDSVKQYTPPGADNSSLTTRI 117
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 LAGCTTGAAVAVCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 180
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 LAGCTTGAAVAVCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPCHFVSAFGACATVVASPVVY 240
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 177 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPCHFVSAFGACATVVASPVVY 236
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 VTRVYNSPPGQYFSPDLCKIMVAOEGPTAFYKGFPSFLRIGSNVNMVFYIEQLKRA 300
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 237 VTRVYNSPPGQYFSPDLCKIMVAOEGPTAFYKGFPSFLRIGSNVNMVFYIEQLKRA 296
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 LMKVQMLRESPPF 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 297 LMKVQMLRESPPF 308
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 8
US-09-172-528-2
Sequence 2, Application US/09172528
Patent No. 5952469

GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-172-528-2
```

```
Query Match      84.5%; Score 1369; DB 2; Length 308;
Best Local Similarity 85.3%; Pred. No. 1,7e-150;
Matches 266; Conservative 18; Mismatches 24; Indels 4; Gaps 2;
```

```
QY 1 MVLGKPSDVPTMAVKFLGAGTAACPADLVTPPLDTAKVRLQIOGENDAVQTARLVQYRG 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MVLGKPSDVPTMAVKFLGAGTAACPADLVTPPLDTAKVRLQIOGENDAVQTARLVQYRG 57
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 VLGITILMTWRTGSPSPVNGVAGLQROMSPASIRIGLVDSVKQYTPPGADNSSLTTRI 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 58 VLGITILMTWRTGSPSPVNGVAGLQROMSPASIRIGLVDSVKQYTPPGADNSSLTTRI 117
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 LAGCTTGAAVAVCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 180
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 LAGCTTGAAVAVCAOPTDVVKVRFQASIHGSPSRDRTSGTMDAYRTIAREGVGLWK 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPCHFVSAFGACATVVASPVVY 240
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 177 GTLPNIRNAIVNCAEVVYDILKEKLDYHLITDNFPCHFVSAFGACATVVASPVVY 236
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 VTRVYNSPPGQYFSPDLCKIMVAOEGPTAFYKGFPSFLRIGSNVNMVFYIEQLKRA 300
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 237 VTRVYNSPPGQYFSPDLCKIMVAOEGPTAFYKGFPSFLRIGSNVNMVFYIEQLKRA 296
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 LMKVQMLRESPPF 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 297 LMKVQMLRESPPF 308
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 9
US-09-318-199-2
Sequence 2, Application US/09318199
Patent No. 6025469

GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,466
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 432 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-937-466-4

Query Match 82.8%; Score 1341; DB 2; Length 432;
 Best Local Similarity 85.6%; Pred. No. 5.1e-147;
 Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 MVGLRSDVPTMVKFLGAGTACFADLVTPPLDTAKRLQIOGENOVAQTARLVQYRG 60
 DB 1 MVGLRSDVPTMVKFLGAGTACFADLVTPPLDTAKRLQIOGENOVAQTARLVQYRG 57
 QY 61 VLGITLTVWRTGPGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYTTKGDNSLTTRI 120
 DB 58 VLGITLTVWRTGPGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYTTKGDNSLTTRI 117
 QY 121 LAGCTGMAVTCAPTDVVVVRPQASIHLPSSDRKSGTMDYRTIAREEGVRLMK 180
 DB 118 LAGCTGMAVTCAPTDVVVVRPQASIHLPSSDRKSGTMDYRTIAREEGVRLMK 176
 QY 181 GTLPINIMENALVNCSEVVTYDILKEKLDYHLTDNPFCHVSAFAGCATVVASPDV 240
 DB 177 GTWPIITRNALVNCSEVVTYDILKEKLDYHLTDNPFCHVSAFAGCATVVASPDV 236
 QY 241 VKTRYNMSPPGQYFSPDLDMIRVAQEGPTAFYKGFPSFLRLGSMNVMFTYEQLKRA 300
 DB 237 VKTRYNMSPPGQYFSPDLDMIRVAQEGPTAFYKGFPSFLRLGSMNVMFTYEQLKRA 296
 QY 301 LMKVQ 305
 DB 297 LMKVQ 301

RESULT 12
 US-09-172-528-4
 Sequence 4, Application US/09172528
 Patent No. 5952469
 GENERAL INFORMATION:
 APPLICANT: Zhang, Ning
 APPLICANT: Amaral, M. Catherine
 APPLICANT: Chen, Jin-Long
 TITLE OF INVENTION: UCP3 Genes
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/172,528
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/937,466
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 432 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-172-528-4

Query Match 82.8%; Score 1341; DB 2; Length 432;
 Best Local Similarity 85.6%; Pred. No. 5.1e-147;
 Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 MVGLRSDVPTMVKFLGAGTACFADLVTPPLDTAKRLQIOGENOVAQTARLVQYRG 60
 DB 1 MVGLRSDVPTMVKFLGAGTACFADLVTPPLDTAKRLQIOGENOVAQTARLVQYRG 57
 QY 61 VLGITLTVWRTGPGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYTTKGDNSLTTRI 120
 DB 58 VLGITLTVWRTGPGSPYNGVLVAGLQROMSPASIRIGLYDSVKQYTTKGDNSLTTRI 117
 QY 121 LAGCTGMAVTCAPTDVVVVRPQASIHLPSSDRKSGTMDYRTIAREEGVRLMK 180
 DB 118 LAGCTGMAVTCAPTDVVVVRPQASIHLPSSDRKSGTMDYRTIAREEGVRLMK 176
 QY 181 GTLPINIMENALVNCSEVVTYDILKEKLDYHLTDNPFCHVSAFAGCATVVASPDV 240
 DB 177 GTWPIITRNALVNCSEVVTYDILKEKLDYHLTDNPFCHVSAFAGCATVVASPDV 236
 QY 241 VKTRYNMSPPGQYFSPDLDMIRVAQEGPTAFYKGFPSFLRLGSMNVMFTYEQLKRA 300
 DB 237 VKTRYNMSPPGQYFSPDLDMIRVAQEGPTAFYKGFPSFLRLGSMNVMFTYEQLKRA 296
 QY 301 LMKVQ 305
 DB 297 LMKVQ 301

RESULT 13
 US-09-318-199-4
 Sequence 4, Application US/09318199
 Patent No. 6025469
 GENERAL INFORMATION:
 APPLICANT: Zhang, Ning
 APPLICANT: Amaral, M. Catherine
 APPLICANT: Chen, Jin-Long
 TITLE OF INVENTION: UCP3 Genes
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/318,199
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-318-199-4

Query Match 82.8%; Score 1341; DB 3; Length 432;
Best Local Similarity 85.6%; Pred. No. 5,1e-147;
Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 MVLKPSDVEPTNAVFLGAGTACFADLTVPFLDTAKVRLQIGENQAVQTRALVQYRG 60
DB 1 MVLGQSEVPPTTVKFLGAGTACFADLTVPFLDTAKVRLQIGENQAVQTRALVQYRG 57
QY 61 VLCTILLMTWTEPCSPYNGLVAGLORQMSPASIRIGLVDSVQVTPPKADNSLTTRI 120
DB 58 VLCTILLMTWTEPCSPYNGLVAGLORQMSPASIRIGLVDSVQVTPPKADNSLTTRI 117
QY 121 LAGCTGAMAVTCAOPTDVKKVRFQASIHGPRSDRKSQTMAYRTIAREEGVRLMK 180
DB 118 LAGCTGAMAVTCAOPTDVKKVRFQAMIRLG-TGGERKYGTMAYRTIAREEGVRLMK 176
QY 181 GLTLENIRNAIVNCAEVYTDILKEKLDYHLTDNPFCHVSAFGAFCAIVVSPDV 240
DB 177 GTWPNITRNALIVNCAEVYTDILKEKLBESHLFTDNPFCHVSAFGAFCAIVVSPDV 236
QY 241 VKTRYNMSPGQYFSPDLCMKIKNVAQSGPTAFYKGFPSFLRIGSNVVMFVTEQLKRA 300
DB 237 VKTRYNMSPGQYFSPDLCMKIKNVAQSGPTAFYKGFPSFLRIGSNVVMFVTEQLKRA 296
QY 301 LMKVQ 305
DB 297 LMKVQ 301

RESULT 14
US-09-503-579-4
Sequence 4, Application US/09503579
Patent No. 6248561
GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,579
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-503-579-4

Query Match 82.8%; Score 1341; DB 3; Length 432;
Best Local Similarity 85.6%; Pred. No. 5,1e-147;
Matches 261; Conservative 17; Mismatches 23; Indels 4; Gaps 2;

QY 1 MVLKPSDVEPTNAVFLGAGTACFADLTVPFLDTAKVRLQIGENQAVQTRALVQYRG 60
DB 1 MVLGQSEVPPTTVKFLGAGTACFADLTVPFLDTAKVRLQIGENQAVQTRALVQYRG 57
QY 61 VLCTILLMTWTEPCSPYNGLVAGLORQMSPASIRIGLVDSVQVTPPKADNSLTTRI 120
DB 58 VLCTILLMTWTEPCSPYNGLVAGLORQMSPASIRIGLVDSVQVTPPKADNSLTTRI 117
QY 121 LAGCTGAMAVTCAOPTDVKKVRFQASIHGPRSDRKSQTMAYRTIAREEGVRLMK 180
DB 118 LAGCTGAMAVTCAOPTDVKKVRFQAMIRLG-TGGERKYGTMAYRTIAREEGVRLMK 176
QY 181 GLTLENIRNAIVNCAEVYTDILKEKLDYHLTDNPFCHVSAFGAFCAIVVSPDV 240
DB 177 GTWPNITRNALIVNCAEVYTDILKEKLBESHLFTDNPFCHVSAFGAFCAIVVSPDV 236
QY 241 VKTRYNMSPGQYFSPDLCMKIKNVAQSGPTAFYKGFPSFLRIGSNVVMFVTEQLKRA 300
DB 237 VKTRYNMSPGQYFSPDLCMKIKNVAQSGPTAFYKGFPSFLRIGSNVVMFVTEQLKRA 296
QY 301 LMKVQ 305
DB 297 LMKVQ 301

RESULT 15
US-10-001-051B-2
Sequence 2, Application US/10001051B
Patent No. 6670138
GENERAL INFORMATION:
APPLICANT: Gonzalez-Zulueta, Mirella
APPLICANT: Shamloo, Mehrdad
APPLICANT: McFarland, K.C.
APPLICANT: Chin, Daniel
APPLICANT: Mieloch, Tadeusz
APPLICANT: Welcher, Thorsten
APPLICANT: AGY Therapeutics, Inc.
TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
FILE REFERENCE: 019488-003010US

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:53:27 ; Search time 48 seconds
(without alignments)
1808.699 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620
Sequence: 1 MVGLKPSDVPPTMAVKFLG.....TYQLKRLMKYQMLRESPE 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/2/pubppaa/PC7US_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*

16: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
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| 2 | 1620 | 100.0 | 312 | 9 | US-09-826-507-2 |
| 3 | 1620 | 100.0 | 312 | 9 | US-09-808-457-2 |
| 4 | 1620 | 100.0 | 312 | 12 | US-10-671-628-9 |
| 5 | 1556 | 96.0 | 309 | 14 | US-10-270-861-35 |
| 6 | 1430 | 88.3 | 275 | 9 | US-09-808-457-4 |
| 7 | 1430 | 88.3 | 284 | 10 | US-09-823-886A-6 |
| 8 | 1152.5 | 71.1 | 309 | 9 | US-09-884-814-8 |
| 9 | 1152.5 | 71.1 | 309 | 13 | US-10-001-051B-2 |
| 10 | 1152.5 | 71.1 | 309 | 15 | US-10-197-019-3 |
| 11 | 1149.5 | 71.0 | 309 | 9 | US-09-884-814-1 |
| 12 | 1149.5 | 71.0 | 309 | 12 | US-10-336-472-132 |
| 13 | 1149.5 | 71.0 | 309 | 12 | US-10-671-628-8 |
| 14 | 1149.5 | 71.0 | 309 | 14 | US-10-270-861-34 |
| 15 | 1149.5 | 71.0 | 309 | 14 | US-10-265-689-1 |

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|----|--------|------|-----|----|----------------------|-------------------|
| 16 | 1149.5 | 71.0 | 314 | 10 | US-09-823-886A-4 | Sequence 4, Appli |
| 17 | 1147.5 | 70.8 | 309 | 9 | US-09-884-814-6 | Sequence 6, Appli |
| 18 | 1142.5 | 70.5 | 321 | 12 | US-10-336-472-130 | Sequence 130, App |
| 19 | 919 | 56.7 | 306 | 12 | US-10-037-417-89 | Sequence 89, Appl |
| 20 | 910.5 | 56.2 | 307 | 10 | US-09-823-886A-2 | Sequence 2, Appli |
| 21 | 910.5 | 56.2 | 307 | 12 | US-10-037-417-87 | Sequence 87, Appl |
| 22 | 905 | 55.9 | 306 | 12 | US-10-037-417-90 | Sequence 88, Appl |
| 23 | 902.5 | 55.7 | 307 | 12 | US-10-037-417-88 | Sequence 7, Appli |
| 24 | 902.5 | 55.7 | 307 | 12 | US-10-671-628-7 | Sequence 33, Appl |
| 25 | 902.5 | 55.7 | 307 | 14 | US-10-270-861-33 | Sequence 91, Appl |
| 26 | 873.5 | 53.9 | 307 | 12 | US-10-037-417-91 | Sequence 26, Appl |
| 27 | 736.5 | 45.5 | 271 | 12 | US-10-037-417-26 | Sequence 5, Appli |
| 28 | 687 | 42.4 | 306 | 12 | US-10-671-628-5 | Sequence 6317, A |
| 29 | 681.5 | 42.1 | 345 | 12 | US-10-425-114-65317 | Sequence 237696, |
| 30 | 676 | 41.7 | 305 | 12 | US-10-424-599-237696 | Sequence 2, Appli |
| 31 | 675.5 | 41.7 | 303 | 12 | US-10-671-628-2 | Sequence 4, Appli |
| 32 | 651 | 40.2 | 314 | 12 | US-10-671-628-6 | Sequence 6, Appli |
| 33 | 592 | 36.5 | 268 | 12 | US-10-671-628-4 | Sequence 11, Appl |
| 34 | 521 | 32.2 | 322 | 14 | US-10-270-861-11 | Sequence 13, Appl |
| 35 | 521 | 32.2 | 325 | 14 | US-10-270-861-13 | Sequence 7, Appli |
| 36 | 512 | 31.6 | 322 | 14 | US-10-270-861-7 | Sequence 118, App |
| 37 | 512 | 31.6 | 325 | 14 | US-10-270-861-1 | Sequence 152, App |
| 38 | 512 | 31.6 | 335 | 10 | US-09-984-271-118 | Sequence 2476, Ap |
| 39 | 512 | 31.6 | 335 | 12 | US-10-262-511-152 | Sequence 276094, |
| 40 | 509 | 31.4 | 325 | 12 | US-09-984-271-118 | Sequence 276095, |
| 41 | 500.5 | 30.9 | 291 | 15 | US-10-108-260A-2476 | Sequence 52234, A |
| 42 | 496.5 | 30.6 | 317 | 12 | US-10-424-599-276094 | Sequence 9, Appli |
| 43 | 487.5 | 30.1 | 341 | 12 | US-10-425-114-52234 | |
| 44 | 487.5 | 30.1 | 341 | 12 | US-10-425-114-52234 | |
| 45 | 486.5 | 30.0 | 353 | 14 | US-10-270-861-9 | |

ALIGNMENTS

RESULT 1

US-09-734-134-2

Sequence 2, Application US/09734134

Patent No. US20010010929A1

GENERAL INFORMATION:

APPLICANT: Lee James Bealey

APPLICANT: Robert James Godden

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GB-30002-D1

CURRENT APPLICATION NUMBER: US/09/734,134

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: GB 9704551.2

PRIOR FILING DATE: 1997-03-05

PRIOR APPLICATION NUMBER: GB 9705614.7

PRIOR FILING DATE: 1997-03-18

PRIOR APPLICATION NUMBER: EP 97305305.1

PRIOR FILING DATE: 1997-07-16

PRIOR APPLICATION NUMBER: GB 9800633

PRIOR FILING DATE: 1998-03-02

PRIOR APPLICATION NUMBER: 09/142,565

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-734-134-2

Query Match 100.0%; Score 1620; DB 9; Length 312;

Best Local Similarity 100.0%; Pred. No. 2.2e-157;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MVGLKPSDVPPTMAVKFLGAGTAACFADLVFPPLDTAKVRLIOGENQAVQTAFLVQYRG 60

| | | | |
|----|-----|--|-----|
| QY | 61 | VAGTLLTWRETEGPGSPNGVLVAGIOROMSPASIRGLDVSQOYTTPKGADNSSLTTTR | 120 |
| Dd | 61 | VAGTLLTWRETEGPGSPNGVLVAGLORQMSPASIRGLDVSQOYTTPKGADNSSLTTTR | 120 |
| QY | 121 | LACGTGGAAVTCAPPTDVKVRFOASIHLSGRSDRKYSGMTDAYRTIAREEGVGWLK | 180 |
| Dd | 121 | LACGTGGAAVTCAPPTDVKVRFOASHLGSRSDRKYSGMTDAYRTIAREEGVGWLK | 180 |
| QY | 181 | GTLPIPMNAAYNCAEVVTYDILKEGLDLHYLLTDNPFCHPUSAFAAGCATVVASPVUV | 240 |
| Dd | 181 | GTLPIPMNAAYNCAEVVTYDILKEGLDLHYLLTDNPFCHPUSAFAGCATVVASPVUV | 240 |
| QY | 241 | VKTIRYMNSPPGOYFSPPLDCMIMOVAOEGPTAFYKGPBFLRLGSNNVMVFVTEQLKA | 300 |
| Dd | 241 | VKTIRYMNSPPGOYFSPPLDCMIMOVAOEGPTAFYKGPBFLRLGSNNVMVFVTEQLKA | 300 |
| QY | 301 | LMKVQMLRESPP | 312 |
| Dd | 301 | LMKVQMLRESPP | 312 |

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RESULT 2
US-09-826-507-2
Sequence 2, Application US/09826507
Patent No. US20020004492A1
GENERAL INFORMATION:
APPLICANT: Lee James Beesley
APPLICANT: John Christopher Clapham
APPLICANT: Robert James Godden
TITLE OF INVENTION: NEW USE
FILE REFERENCE: GH-30009-C1
CURRENT APPLICATION NUMBER: US/09/826,507
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/312,620
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 9814926.3
PRIOR FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-826-507-2

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| Query Match | 100.0% | Score 1620 | DB 9 | Length 312 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 100.0% | Pred. No. 2.2e-167 | | |
| Matches 312 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | MVGLKPSDVPPTMAVKFLGAGTAACFADIVTTPPLDTAKRLQIOGNNQAVQTARLVQYRG | 60 | |
| Db | 1 | MVGLKPSDVPPTMAVKFLGAGTAACFADIVTTPPLDTAKRLQIOGNNQAVQTARLVQYRG | 60 | |
| QY | 61 | VLGTLITLWRTGSPSPYNGLVAGLQRONSPASIRIGLYDSVKQYVTPKQADNSLITRI | 120 | |
| Db | 61 | VLGTLITLWRTGSPSPYNGLVAGLQRONSPASIRIGLYDSVKQYVTPKQADNSLITRI | 120 | |
| QY | 121 | LAGCTTGMAVTCAPPTDVVKYRFOASIHLSGSRSPRKSGTMDAVRTIARBSGVRLMK | 180 | |
| Db | 121 | LAGCTTGMAVTCAPPTDVVKYRFOASIHLSGSRSPRKSGTMDAVRTIARBSGVRLMK | 180 | |
| QY | 181 | GTLPIIMRAIYNCAQEVVYYTLIKELDLBYHLITDNFPCGFVSAFQAGCFCAVVASPVVDV | 240 | |
| Db | 181 | GTLPIIMRAIYNCAQEVVYYTLIKELDLBYHLITDNFPCGFVSAFQAGCFCAVVASPVVDV | 240 | |
| QY | 241 | VKTRVNNSPGGYFSPFLDCMIRKQVAGSGPTAFYKGFPSFLRIGSNVNVFVYYEQLKRA | 300 | |
| Db | 241 | VKTRVNNSPGGYFSPFLDCMIRKQVAGSGPTAFYKGFPSFLRIGSNVNVFVYYEQLKRA | 300 | |
| QY | 301 | LMKVQMLRESPP 312 | | |
| Db | 301 | LMKVQMLRESPP 312 | | |

```

RESULT 3
US-09-808-457-2
: Sequence 2, Application US/09808457
: Patent No. US20020065239A1
: GENERAL INFORMATION:
: APPLICANT: Boettcher, Brian
: APPLICANT: Caplan, Shari
: APPLICANT: Kaleko, Michael
: APPLICANT: Connolly, Sheila
: APPLICANT: Desai, Urv
: APPLICANT: Slosberg, Eric
: TITLE OF INVENTION: Methods and Compositions For Treatment
: TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy
: FILE REFERENCE: 4-31353A/USN
: CURRENT APPLICATION NUMBER: US/09/808,457
: CURRENT FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 60/XXX,XXX
: PRIOR FILING DATE: 2000-03-15
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 312
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Protein UCP3L
US-09-808-457-2

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OTHER INFORMATION: Protein UCP3L
US-09-808-457-2

| Query Match | Score | DB | Length |
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| 100.0% | 1620 | 9 | 312 |

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

| | | | |
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| QY | 1 | MVGLKPSVPEPTMAVKFLLGAGTAACAFALUNPPLDTAVKRLQIQENQAVQTAARLVQYXG | 60 |
| Db | 1 | MVGLKPSVPEPTMAVKFLLGAGTAACAFALVTFPLDTAKRLQIQENQAVQTAARLVQYXG | 60 |
| QY | 61 | VLGITLTVNRLEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKOYVTPKCADNSSLTTRI | 120 |
| Db | 61 | VLGITLTVNRLEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKOYVTPKCADNSSLTTRI | 120 |
| QY | 121 | LAGCTTGAMAATCAQPTDVVKVRFQASIHLSGRSDRKYSGTMDAYRTIAREEGVGLWK | 180 |
| Db | 121 | LAGCTTGAMAATCAQPTDVVKVRFQASIHLSGRSDRKYSGTMDAYRTIAREEGVGLWK | 180 |
| QY | 181 | GTLPEINMANAVNCABEVTTDILKEKLIDYHLLTDFPCHFIASAGAGCAIVVASPVUV | 240 |
| Db | 181 | GTLPEINMANAVNCABEVTTDILKEKLIDYHLLTDFPCHFIASAFAGCAIVVASPVUV | 240 |
| QY | 241 | VKTRVMSPPGQYRSPDLDCMKMAQOEGPTAFYKGFPSFLRLGSMNVVMFTYBEOLKRA | 300 |
| Db | 241 | VKTRVMSPPGQYRSPDLDCMKMAQOEGPTAFYKGFPSFLRLGSMNVVMFTYBEOLKRA | 300 |
| QY | 301 | LMKVQMLRESPF 312 | |
| Db | 301 | LMKVQMLRESPF 312 | |

RESULT 4
US-10-671-628-9
Sequence 9, Application US/10671628
Publication No. US20040068105A1
GENERAL INFORMATION:
APPLICANT: TTO, Kikukatsu
TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
FILE REFERENCE: 2003-1386A/MMC/00653
CURRENT APPLICATION NUMBER: US-10/671.628
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: 10/009,962
PRIOR FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: PCT/JP00/03806
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: JP11-167439

PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-10-671-628-9

Query Match 100.0%; Score 1620; DB 12; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MVLGKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRG 60
QY 61 VLGTILTMVTEGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120
DB 61 VLGTILTMVTEGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120
QY 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSRKSGTMDAYRTIAREEGVRLMK 180
DB 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSRKSGTMDAYRTIAREEGVRLMK 180
QY 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDV 240
DB 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDV 240
QY 241 VKTRYNNSPPQYFSPIDCMIKMVAQEGPTAFYKGFPSFRLGSMNVVMFVTEQLKRA 300
DB 241 VKTRYNNSPPQYFSPIDCMIKMVAQEGPTAFYKGFPSFRLGSMNVVMFVTEQLKRA 300
QY 301 LMKVQMLRESPE 312
DB 301 LMKVQMLRESPE 312

RESULT 5

US-10-270-861-35
Sequence 35, Application US/10270861
Publication No. US2003007749A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Adams, Sean
TITLE OF INVENTION: UCP5
FILE REFERENCE: P1663R2
CURRENT APPLICATION NUMBER: US/10/270, 861
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US/09/433, 622
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: US 60/110, 286
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: US 60/129, 583
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: US 60/143, 886
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 35
LENGTH: 300
TYPE: PRT
ORGANISM: Homo Sapien
US-10-270-861-35

Query Match 96.0%; Score 1556; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.9e-160;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MAVFELAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRGVLTILTMVTE 72
DB 1 MAVFELAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRGVLTILTMVTE 60
QY 73 GPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGADNSLTTRIAGCTGAMAVT 132

DB 61 GPCSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGADNSLTTRIAGCTGAMAVT 120
QY 133 CAOPTDVVKVRFQASIHGSPSRSRKSGTMDAYRTIAREEGVRLMKGLPIMIRNAIV 192
DB 121 CAOPTDVVKVRFQASIHGSPSRSRKSGTMDAYRTIAREEGVRLMKGLPIMIRNAIV 180
QY 193 NCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDVVKTRYNNSPPQ 252
DB 181 NCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDVVKTRYNNSPPQ 240
QY 253 YFSPIDCMIKMVAQEGPTAFYKGFPSFRLGSMNVVMFVTEQLKRALMKVQMLRESPE 312
DB 241 YFSPIDCMIKMVAQEGPTAFYKGFPSFRLGSMNVVMFVTEQLKRALMKVQMLRESPE 300

RESULT 6

US-09-808-457-4
Sequence 4, Application US/09808457
Patent No. US20020065239A1
GENERAL INFORMATION:
APPLICANT: Boettcher, Brian
APPLICANT: Caplan, Shari
APPLICANT: Kaleko, Michael
APPLICANT: Connolly, Sheila
APPLICANT: Desai, Urvil
APPLICANT: Slosberg, Eric
TITLE OF INVENTION: Methods and Compositions For Treatment
TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy
FILE REFERENCE: 4-31353A/USN
CURRENT APPLICATION NUMBER: US/09/808, 457
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 2001-03-14
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 275
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Protein UCP35
US-09-808-457-4

Query Match 88.3%; Score 1430; DB 9; Length 275;
Best Local Similarity 100.0%; Pred. No. 8.7e-147;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLGKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRG 60
DB 1 MVLGKPSDVPPTMAVKELGAGTAACFADLVTFPLDTAKVRLQIGENQAVQTARLVQYRG 60
QY 61 VLGTILTMVTEGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120
DB 61 VLGTILTMVTEGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKGADNSLTTRI 120
QY 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSRKSGTMDAYRTIAREEGVRLMK 180
DB 121 LAGCTGAMAVTCAQPTDVVKVRFQASIHGSPSRSRKSGTMDAYRTIAREEGVRLMK 180
QY 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDV 240
DB 181 GTLPNIRNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPDV 240
QY 241 VKTRYNNSPPQYFSPIDCMIKMVAQEGPTAFYKGFPSFRLGSMNVVMFVTEQLKRALMKVQMLRESPE 312
DB 241 VKTRYNNSPPQYFSPIDCMIKMVAQEGPTAFYKGFPSFRLGSMNVVMFVTEQLKRALMKVQMLRESPE 300

RESULT 7

US-09-823-886A-6
Sequence 6, Application US/09823886A
Publication No. US20030150022A1

```

GENERAL INFORMATION:
APPLICANT: Berry-Lowe, Sandra
TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
FILE REFERENCE: C1102/7002
CURRENT APPLICATION NUMBER: US/09/823,886A
PRIORITY FILING DATE: 2001-03-30
PRIORITY APPLICATION NUMBER: US 60/193,533
PRIORITY FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in version 3.0
SEQ ID NO 6
LENGTH: 284
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-886A-6

Query Match      88.3%; Score 1430; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 9,1e-147;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60
DB 10 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 69
QY 61 VLGITLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTTRI 120
DB 70 VLGITLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTTRI 129
QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHLAGPSRSDRKYSGMTDAYRTIAREBGVRLGMK 180
DB 130 LAGCTTGAMAVTCAOPTDVVKVRFQASIHLAGPSRSDRKYSGMTDAYRTIAREBGVRLGMK 189
QY 181 GTLENIMRNAINVCAEVYTDILKEKLDYHLITDNFPCHFISAGAGFCATVVASPDV 240
DB 190 GTLENIMRNAINVCAEVYTDILKEKLDYHLITDNFPCHFISAGAGFCATVVASPDV 249
QY 241 VKTIRYNSPPGOYFSPIDCMIKVVAOEGPTAFYKG 275
DB 250 VKTIRYNSPPGOYFSPIDCMIKVVAOEGPTAFYKG 284

RESULT 8
US-09-884-814-8
Sequence 8, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chen, Jin-Long
APPLICANT: Amaral, M. Catherine
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Human uncoupling Protein 2 (hUCP2): Compositions and
TITLE OF INVENTION: Methods of use
FILE REFERENCE: 018781-001110US
CURRENT APPLICATION NUMBER: US/09/884,814
CURRENT FILING DATE: 2001-06-18
PRIORITY APPLICATION NUMBER: US 09/124,293
PRIORITY FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 8
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.
US-09-884-814-8

Query Match      71.1%; Score 1152.5; DB 9; Length 309;
Best Local Similarity 72.2%; Pred. No. 1.6e-116;
Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYR 59
DB 1 MWGLKPSDVPPTMAVKFAGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYR 59

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DB 1 MWGFATDVPPATVVKFAGAGTACIADLITPPLDTAKVRLQIOGESQGPVATASQYR 60
QY 60 GVLGTLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTTRI 119
DB 61 GVMGTLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTTRI 119
QY 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHLAGPSRSDRKYSGMTDAYRTIAREBGVRLGM 179
DB 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHLAGPSRSDRKYSGMTDAYRTIAREBGVRLGM 176
QY 180 KGTLENIMRNAINVCAEVYTDILKEKLDYHLITDNFPCHFISAGAGFCATVVASPDV 239
DB 177 KGTLENIMRNAINVCAEVYTDILKEKLDYHLITDNFPCHFISAGAGFCATVVASPDV 236
QY 240 VKTIRYNSPPGOYFSPIDCMIKVVAOEGPTAFYKGFTSPFLRGSNMVMEVTEYQDKR 299
DB 237 VKTIRYNSPPGOYFSPIDCMIKVVAOEGPTAFYKGFTSPFLRGSNMVMEVTEYQDKR 296
QY 300 ALMKVQLRBSPPF 312
DB 297 ALMAACTSREAPF 309

RESULT 9
US-10-001-051B-2
Sequence 2, Application US/10001051B
Publication No. US20020127958A1
GENERAL INFORMATION:
APPLICANT: Gonzalez-Zulueta, Mirella
APPLICANT: Shamloo, Mehdiad
APPLICANT: McFarland, K. C.
APPLICANT: Chin, Daniel
APPLICANT: Melioch, Tadeusz
APPLICANT: Melcher, Thorsten
APPLICANT: Agt Therapeutics, Inc.
TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
FILE REFERENCE: 019488-003010US
CURRENT APPLICATION NUMBER: US/10/001,051B
CURRENT FILING DATE: 2002-06-25
PRIORITY APPLICATION NUMBER: US 60/244,946
PRIORITY FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 309
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Any animal
OTHER INFORMATION: source, typically mammalian, most typically human
US-10-001-051B-2

Query Match      71.1%; Score 1152.5; DB 13; Length 309;
Best Local Similarity 72.2%; Pred. No. 1.6e-116;
Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFAGAGTACIADLITPPLDTAKVRLQIOGESQGPVATASQYR 59
DB 1 MWGFATDVPPATVVKFAGAGTACIADLITPPLDTAKVRLQIOGESQGPVATASQYR 60
QY 60 GVLGTLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTTRI 119
DB 61 GVMGTLTMVTRTEGPCSPYNGIVAGLQROMSPASIRIGLYDSVKOYVTPPKGADNSLTTTRI 119
QY 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHLAGPSRSDRKYSGMTDAYRTIAREBGVRLGM 179
DB 120 ILAAGCTTGAMAVTCAOPTDVVKVRFQASIHLAGPSRSDRKYSGMTDAYRTIAREBGVRLGM 176
QY 180 KGTLENIMRNAINVCAEVYTDILKEKLDYHLITDNFPCHFISAGAGFCATVVASPDV 239
DB 177 KGTLENIMRNAINVCAEVYTDILKEKLDYHLITDNFPCHFISAGAGFCATVVASPDV 236

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QY 240 VVKTRVNSPPGOYSPPLDCMKVVAOEGPTAFYKGFPSFLRSGMNVMMFTYEQLR 299
 DB 237 VVKTRVNSALGOYSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVMMFTYEQLR 296
 QY 300 ALMKVQMLRESPF 312
 DB 297 ALMAACTSREAPF 309

RESULT 10

US-10-197-019-3
 ; Sequence 3, Application US/10197019
 ; Publication No. US20030207284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Gilson, Christopher Raleigh
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Parks, Katie B.
 ; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
 ; FILE REFERENCE: MMH-004205
 ; CURRENT APPLICATION NUMBER: US/10/197,019
 ; PRIOR FILING DATE: 2002-07-16
 ; PRIOR APPLICATION NUMBER: PCT/US01/02485
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 309
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; US-10-197-019-3

Query Match 71.1%; Score 1152.5; DB 15; Length 309;
 Best Local Similarity 72.2%; Pred. No. 1.5e-116; Indels 5; Gaps 3;

Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;
 QY 1 MYGLKPSDVPPTMAVFLGAGTAACFADLVTPPLDTAKVRLQIQGNQA-VQTAFLVQYR 59
 DB 1 MGFPAKTDVPPATVYKFLGAGTAACIADLITPPLDTAKVRLQIQGSGQVPRATASQYR 60
 QY 60 GVLTGTLTWRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSLITR 119
 DB 61 GVGGLTLTWRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSLITR 119
 QY 120 ILAAGCTTGAMAVTCAOPTDVVKVRPQASIHLSRSDRYSGTMDAYRTIAREEGVRLW 179
 DB 120 LLAGSTTGALAAVNAQPTDVVKVRPQQAQABAG--GGRRYOSTVNAVKTIAREEGVRLW 176
 QY 180 KGTLPNIMNNAIVNCAEVVYDILKEKLDYHLITDNFCHFPVSAGAGFCATVVASPVD 239
 DB 177 KGTSPVARNNAIVNCAELVYDILKDALKAMLTMDLCPCHFTSAGAGCTTVIASPVD 236
 QY 240 VVKTRVNSPPGOYSPPLDCMKVVAOEGPTAFYKGFPSFLRSGMNVMMFTYEQLR 299
 DB 237 VVKTRVNSALGOYSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVMMFTYEQLR 296
 QY 300 ALMKVQMLRESPF 312
 DB 297 ALMAACTSREAPF 309

RESULT 11

US-09-884-814-1
 ; Sequence 1, Application US/09884814
 ; Patent No. US20020127600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
 ; METHODS OF USE
 ; FILE REFERENCE: 018781-001110US

; CURRENT APPLICATION NUMBER: US/09/884,814
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 09/124,293
 ; PRIOR FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 309
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
 ; US-09-884-814-1

Query Match 71.0%; Score 1149.5; DB 9; Length 309;
 Best Local Similarity 72.2%; Pred. No. 3.5e-116;
 Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MYGLKPSDVPPTMAVFLGAGTAACFADLVTPPLDTAKVRLQIQGNQA-VQTAFLVQYR 59
 DB 1 MGFPAKTDVPPATVYKFLGAGTAACIADLITPPLDTAKVRLQIQGSGQVPRATASQYR 60
 QY 60 GVLTGTLTWRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSLITR 119
 DB 61 GVGGLTLTWRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSLITR 119
 QY 120 ILAAGCTTGAMAVTCAOPTDVVKVRPQASIHLSRSDRYSGTMDAYRTIAREEGVRLW 179
 DB 120 LLAGSTTGALAAVNAQPTDVVKVRPQQAQABAG--GGRRYOSTVNAVKTIAREEGVRLW 176
 QY 180 KGTLPNIMNNAIVNCAEVVYDILKEKLDYHLITDNFCHFPVSAGAGFCATVVASPVD 239
 DB 177 KGTSPVARNNAIVNCAELVYDILKDALKAMLTMDLCPCHFTSAGAGCTTVIASPVD 236
 QY 240 VVKTRVNSPPGOYSPPLDCMKVVAOEGPTAFYKGFPSFLRSGMNVMMFTYEQLR 299
 DB 237 VVKTRVNSALGOYSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVMMFTYEQLR 296
 QY 300 ALMKVQMLRESPF 312
 DB 297 ALMAACTSREAPF 309

RESULT 12

US-10-336-472-132
 ; Sequence 132, Application US/10336472
 ; Publication No. US20040043929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Ballinger, Robert A.
 ; APPLICANT: Baumgartner, Jason C.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Chan, John S.
 ; APPLICANT: Bergins, Constance
 ; APPLICANT: Gangolli, Baha A.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Rurak, Katarzyna
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Gilber, Jennifer A.
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Jia, Weizhen
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Paturgajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: MacDougall, John R.

PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: US 60/143,886
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 34
LENGTH: 309
TYPE: PRT
ORGANISM: Homo Sapien
US-10-270-861-34

Query Match 71.0%; Score 1149.5; DB 14; Length 309;
Best Local Similarity 72.2%; Pred. No. 3.5e-116;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MVLKPSDVPPTAVKELGAGTACFADLVTFPLDTAKVRLQIQGSEQGVPRATASQYR 59
DB 1 MVEFKATDVPPTATVTFELGAGTACIADLITFPLDTAKVRLQIQGSEQGVPRATASQYR 60
QY 60 GVLGTTITWRTREGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPPKADNSLITR 119
DB 61 GVMGTTITWRTREGPSRLYNGLVAGLQROMSPASVIRIGLYDSVKQFYT-KGSEHASIGSR 119
QY 120 ILAGCTTGAMAVYCAQPTDVVKVRFQASIHGSRSDRKYSCTMDAYRTIAREEGVRLW 179
DB 120 LLAGSTTGALAVAVAOPTDVVKVRFQAOAPAG--GGRYQSTVNAVKTIAREEGFRGLW 176
QY 180 KGTLPNIMRNAIVNCAEVVYDILKEKLDYHLTDNFPCHFVSAGFCATVVASPVD 239
DB 177 KGTSPVARNALVNCALVYDILKDALIKANLMTDDLPCFTSAFGAGCTTVIASPVD 236
QY 240 VVKTRYNSPPGQYFSPDCKIMVAOEGPTAFYKGFPSFLRGSNNVVMFVYEQDKR 299
DB 237 VVKTRYNSALGGYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRGSNNVVMFVYEQDKR 296
QY 300 ALMKVQMLRESPP 312
DB 297 ALMAACTSREAPF 309

RESULT 15
US-10-265-689-1
Sequence 1, Application US/10265689
Publication No. US20030119775A1
GENERAL INFORMATION:
APPLICANT: SURWIT, RICHARD S.
APPLICANT: COLLINS, SHEILA A.
APPLICANT: WARDEN, CRAIG H.
APPLICANT: SEIDIN, MICHAEL F.
APPLICANT: RICOTER, DANIEL
APPLICANT: BOUILLAUD, FREDERIC
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
FILE REFERENCE: 1579-376
CURRENT APPLICATION NUMBER: US/10/265,689
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/353,645
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: PCT/US97/06864
PRIOR FILING DATE: 1997-04-22
PRIOR APPLICATION NUMBER: 60/034,960
PRIOR FILING DATE: 1997-01-15
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-265-689-1

Query Match 71.0%; Score 1149.5; DB 14; Length 309;
Best Local Similarity 72.2%; Pred. No. 3.5e-116;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;
QY 1 MVLKPSDVPPTAVKELGAGTACFADLVTFPLDTAKVRLQIQGSEQGVPRATASQYR 59

DB 1 MVEFKATDVPPTATVTFELGAGTACIADLITFPLDTAKVRLQIQGSEQGVPRATASQYR 60
QY 60 GVLGTTITWRTREGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPPKADNSLITR 119
DB 61 GVMGTTITWRTREGPSRLYNGLVAGLQROMSPASVIRIGLYDSVKQFYT-KGSEHASIGSR 119
QY 120 ILAGCTTGAMAVYCAQPTDVVKVRFQASIHGSRSDRKYSCTMDAYRTIAREEGVRLW 179
DB 120 LLAGSTTGALAVAVAOPTDVVKVRFQAOAPAG--GGRYQSTVNAVKTIAREEGFRGLW 176
QY 180 KGTLPNIMRNAIVNCAEVVYDILKEKLDYHLTDNFPCHFVSAGFCATVVASPVD 239
DB 177 KGTSPVARNALVNCALVYDILKDALIKANLMTDDLPCFTSAFGAGCTTVIASPVD 236
QY 240 VVKTRYNSPPGQYFSPDCKIMVAOEGPTAFYKGFPSFLRGSNNVVMFVYEQDKR 299
DB 237 VVKTRYNSALGGYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRGSNNVVMFVYEQDKR 296
QY 300 ALMKVQMLRESPP 312
DB 297 ALMAACTSREAPF 309

Search completed: May 17, 2004, 11:59:18
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:49:15 ; Search time 59 Seconds
(without alignments)
1494.150 Million cell updates/sec

Title: US-09-423-410-4
Perfect score: 1620
Sequence: 1 MVGLKPSDVPPTMAVKFLGA.....TYEQLKALMKYQWLRESPP 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_230a04:
1: geneeqp1980s:
2: geneeqp1990s:
3: geneeqp2000s:
4: geneeqp2001s:
5: geneeqp2002s:
6: geneeqp2003as:
7: geneeqp2003bs:
8: geneeqp2004s:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1620 | 100.0 | 312 | 2 | AAW83379 Human unc |
| 2 | 1620 | 100.0 | 312 | 2 | AAW68197 Human unc |
| 3 | 1620 | 100.0 | 312 | 2 | AAW85667 Human UCP |
| 4 | 1620 | 100.0 | 312 | 2 | AAW88279 Human unc |
| 5 | 1620 | 100.0 | 312 | 2 | AAW31904 Human unc |
| 6 | 1620 | 100.0 | 312 | 3 | AAW54600 Amino act |
| 7 | 1620 | 100.0 | 312 | 3 | AAW44253 Human mlt |
| 8 | 1620 | 100.0 | 312 | 4 | AAW74296 Human UCP |
| 9 | 1620 | 100.0 | 312 | 4 | AAW04298 Human unc |
| 10 | 1620 | 100.0 | 312 | 5 | AAW68050 Amino act |
| 11 | 1620 | 100.0 | 312 | 5 | AAW81610 UCP3L pro |
| 12 | 1620 | 100.0 | 312 | 7 | AAW19348 Human mlt |
| 13 | 1620 | 100.0 | 312 | 7 | AAW54391 Human Pto |
| 14 | 1616 | 99.8 | 312 | 2 | AAW81587 Human unc |
| 15 | 1610 | 99.4 | 312 | 2 | AAW81588 Protein e |
| 16 | 1430 | 88.3 | 275 | 3 | AAW3380 Human unc |
| 17 | 1430 | 88.3 | 275 | 3 | AAW44293 Human unc |
| 18 | 1430 | 88.3 | 275 | 4 | AAW72343 Human unc |
| 19 | 1430 | 88.3 | 275 | 5 | AAW81611 UCP3S pro |
| 20 | 1430 | 88.3 | 284 | 4 | AAW09078 Human unc |
| 21 | 1426 | 88.0 | 275 | 2 | AAW81591 Human unc |
| 22 | 1403.5 | 86.6 | 339 | 2 | AAW81592 Protein e |
| 23 | 1373 | 84.8 | 308 | 2 | AAW81595 Mouse unc |
| 24 | 1373 | 84.8 | 308 | 2 | AAW88280 Mouse unc |
| 25 | 1369 | 84.5 | 308 | 2 | AAW29834 Mouse unc |

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 1369 | 84.5 | 308 | 2 | AAW85116 | AAW85116 A murine |
| 27 | 1369 | 84.5 | 308 | 4 | AAW77452 | AAW77452 Murine mi |
| 28 | 1369 | 84.5 | 308 | 4 | AAW04729 | AAW04729 Mouse unc |
| 29 | 1366 | 84.3 | 397 | 2 | AAW81596 | AAW81596 Protein e |
| 30 | 1341 | 82.8 | 432 | 2 | AAW29835 | AAW29835 Mouse unc |
| 31 | 1341 | 82.8 | 432 | 2 | AAW85117 | AAW85117 A murine |
| 32 | 1341 | 82.8 | 432 | 3 | AAW77453 | AAW77453 Murine mi |
| 33 | 1341 | 82.8 | 432 | 4 | AAW04730 | AAW04730 Mouse unc |
| 34 | 1156.5 | 71.4 | 309 | 7 | AAW54389 | AAW54389 Rat Prote |
| 35 | 1152.5 | 71.1 | 309 | 2 | AAW69166 | AAW69166 Human tes |
| 36 | 1152.5 | 71.1 | 309 | 2 | AAW28352 | AAW28352 UCP2 amn |
| 37 | 1152.5 | 71.1 | 309 | 5 | AAW98901 | AAW98901 Human unc |
| 38 | 1149.5 | 71.0 | 309 | 2 | AAW28351 | AAW28351 UCP2 amn |
| 39 | 1149.5 | 71.0 | 309 | 2 | AAW31903 | AAW31903 Human unc |
| 40 | 1149.5 | 71.0 | 309 | 3 | AAW44292 | AAW44292 Human unc |
| 41 | 1149.5 | 71.0 | 309 | 3 | AAW45002 | AAW45002 Tularik h |
| 42 | 1149.5 | 71.0 | 309 | 4 | AAW72342 | AAW72342 Human unc |
| 43 | 1149.5 | 71.0 | 314 | 4 | AAW09077 | AAW09077 Human unc |
| 44 | 1147.5 | 70.8 | 309 | 2 | AAW24000 | AAW24000 Complete |
| 45 | 1147.5 | 70.8 | 309 | 2 | AAW89546 | AAW89546 Full leng |

ALIGNMENTS

RESULT 1
AAW83379
ID AAW83379 standard; protein; 312 AA.

AC AAW83379;

DT 22-FEB-1999 (first entry)

DE Human uncoupling protein UCP3L.

Human; uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;
adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;
thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;
insulin sensitivity; neuromuscular disease.

OS Homo sapiens.

PN MO9850542-AL.

PD 12-NOV-1998.

PF 05-MAY-1998; 98WO-EP002645.

PR 07-MAY-1997; 97CH-00001072.

PA (NOVS) NOVARTIS AG.
(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Giacobino J, Muzzin P, Boes O;

DR WPI, 1998-610382/51.

DR N-PSDB; AAW72690.

PT New human skeletal muscle uncoupling proteins UCP3L and UCP3S - useful
for controlling thermogenesis in human skeletal muscle and heart, e.g.
for treating obesity and cachexia.

PS Claim 5, Page 15-16; 26pp; English.

XX The present sequence represents human uncoupling protein UCP3L. UCP3
XX uncouples oxidative phosphorylation and synthesis of adenosine
XX triphosphate in the mitochondria of skeletal muscle. The coding sequences
XX for UCP3L and UCP3S are useful for gene therapy of dysfunctions of
XX thermogenesis in human skeletal muscle and heart which result from a lack
XX of UCP3 and which can induce disorders such as obesity or cachexia.
XX Antisense oligonucleotides to UCP3L and UCP3S can be used for correcting
XX an excess of UCP3. Modification of endogenous UCP3 activity (using
XX activators or inhibitors of UCP3) is used to induce bodyweight loss (loss

CC of adipose mass and maintenance of the lean mass) in all types of obesity
 CC by promoting the dissipation of energy; for preventing an excessive
 CC weight regain following restrictive food diet or after ceasing a physical
 CC training programme; for preventing and treating type II diabetes by
 CC improving sensitivity to insulin; for preventing hypertension; for
 CC increasing muscle mass in states of cachexia; for treatment of
 CC insufficiencies or disturbances of cardiac rhythm due to a dysfunction of
 CC UCP3; and for the treatment of neuromuscular diseases due to a
 CC dysfunction of UCP3. The uncoupling proteins can also be used to raise
 CC antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows
 CC generation of transgenic animals, e.g. for screening substances which
 CC modify UCP3 expression or activity or for investigating the biological
 CC role of UCP3

CC Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 2; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2.2e-165;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKRLQIOGENQAVQTARLVQYRG 60
 DB 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKRLQIOGENQAVQTARLVQYRG 60
 QY 61 VLGITLTWVRETEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSSLTTRI 120
 DB 61 VLGITLTWVRETEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSSLTTRI 120
 QY 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180
 DB 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180
 QY 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVYV 240
 DB 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVYV 240
 QY 241 VKTRYMNSPPQGYFSPFLDCMIKVAQEGPTAFYKGFPSFLRLGSMNVVMFTYEQLKRA 300
 DB 241 VKTRYMNSPPQGYFSPFLDCMIKVAQEGPTAFYKGFPSFLRLGSMNVVMFTYEQLKRA 300
 QY 301 LMKVQMLRESPP 312
 DB 301 LMKVQMLRESPP 312

RESULT 2

ID AAM68197 standard; protein, 312 AA.

AC AAM68197;

DT 07-DEC-1998 (first entry)

DE Human uncoupling protein HNF6W60.

KM HNF6W60; uncoupling protein; human; body weight disorder; obesity;

KW diabetes; hyperlipidaemia; diagnosis; therapy; vaccine.

OS Homo sapiens.

PN WO9839432-A1.

PD 11-SEP-1998.

PP 02-MAR-1998; 98WO-GB000633.

PR 05-MAR-1997; 97GB-00004551.

PR 18-MAR-1997; 97GB-00005614.

PR 16-JUL-1997; 97EP-00305305.

PA (SMK) SMITHKLINE BEECHAM PLC.

XX Beeley LJ, Paine K, Godden RJ;

XX WPI; 1998-495841/42.
 DR N-PSDB; AAV54602.
 XX
 PT New isolated human uncoupling poly(peptide)s - used to develop products
 PT for the diagnosis, prevention and treatment of body weight disorders,
 PT obesity and diabetes.

PS Claim 4; Page 24-25; 41pp; English.

CC This is the amino acid sequence of novel human uncoupling protein
 CC HNF6W60, as deduced from an isolated polynucleotide (see AAV54602). The
 CC invention relates to HNF6W60 polypeptides and recombinant materials and
 CC methods for their production. It also relates to methods for using such
 CC HNF6W60 polypeptides and polynucleotides. Such uses include the treatment
 CC of obesity, diabetes, hyperlipidaemia and body weight disorders. The
 CC invention also provides methods of identifying agonists and antagonists,
 CC and methods for treating conditions associated with HNF6W60 imbalance
 CC using the identified compounds. In addition, diagnostic assays for
 CC detecting diseases associated with inappropriate HNF6W60 activity or
 CC levels are provided

CC Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 2; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2.2e-165;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKRLQIOGENQAVQTARLVQYRG 60
 DB 1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTPPLDTAKRLQIOGENQAVQTARLVQYRG 60
 QY 61 VLGITLTWVRETEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSSLTTRI 120
 DB 61 VLGITLTWVRETEGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYTPKADNSSLTTRI 120
 QY 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180
 DB 121 LAGCTGMAAVTCAOPTDVVKVRFOASIHLPSSDRKYSGTMDAYRTIAREEGVGLMK 180
 QY 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVYV 240
 DB 181 GTLPNIMRNALVNCAEVVTYDILKEKLDYHLTDNPFCHFYSAFGAFCAIVVASPVYV 240
 QY 241 VKTRYMNSPPQGYFSPFLDCMIKVAQEGPTAFYKGFPSFLRLGSMNVVMFTYEQLKRA 300
 DB 241 VKTRYMNSPPQGYFSPFLDCMIKVAQEGPTAFYKGFPSFLRLGSMNVVMFTYEQLKRA 300
 QY 301 LMKVQMLRESPP 312
 DB 301 LMKVQMLRESPP 312

RESULT 3

ID AAM85667 standard; protein, 312 AA.

AC AAM85667;

DT 19-JUL-1999 (first entry)

DE Human UCP-3 (uncoupling protein).

KM UCP-3; uncoupling protein; thermogenesis; skeletal muscle; treatment;

KW obesity; diabetes; hyperthermia; fever; detection; diagnosis.

OS Homo sapiens.

PN WO9845313-A1.

PD 15-OCT-1998.

PP 25-MAR-1998; 98WO-US005892.

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XX 04-APR-1997; 97US-0043407P.
PR 08-MAY-1997; 97US-0046154P.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX Larkin S, Moore C, Albrandt K, Young A, Beaumont K;
XX WPI; 1999-131682/11.
XX N-PSDB; AAX08507.
XX
XX New isolated uncoupling protein, UCP3 - used to develop products for
XX modulating thermogenesis in tissues, e.g. for treating obesity, diabetes,
XX malignant hyperthermia or fever.
XX
XX Claim 4; Fig 5; 97p; English.
XX
XX The uncoupling protein UCP-3 is involved in thermogenesis and energy
XX utilisation in skeletal muscle. The nucleic acid molecule encoding UCP-3
XX or compounds which activate UCP-3 can be used to increase thermogenesis
XX in a subject, e.g. for treating obesity or for decreasing the amount of
XX fat in a subject. They can also be used for treating diabetes. Compound
XX which inhibit UCP-3 activation in tissues of a subject can be used for
XX decreasing thermogenesis or respiratory ATP synthesis e.g. for preventing
XX or treating malignant hyperthermia or fever. The UCP-3 can also be used
XX for screening for compounds that bind to or modulate the activity of UCP-
XX 3, these compounds can then be used in detection and diagnosis
XX
XX Sequence 312 AA;
XX
XX Query Match 100.0%; Score 1620; DB 2; Length 312;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-165;
XX Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MGLKPSDVPPTMAVVFGLGAGTACPADLVTPPLDTAKVRLQIGENQAVQTARLVQYRG 60
XX |||||
XX 1 MGLKPSDVPPTMAVVFGLGAGTACPADLVTPPLDTAKVRLQIGENQAVQTARLVQYRG 60
XX
XX 61 VGTGTLTWTRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPKGDNSLTTR 120
XX |||||
XX 61 VGTGTLTWTRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPKGDNSLTTR 120
XX
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX |||||
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX
XX 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX |||||
XX 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX
XX 241 VKTRYNNSPPGOYFSPDLCMIKXVAOEGPTAFYKGFPSFLRLGSMNVVMFTYBOLK 300
XX |||||
XX 241 VKTRYNNSPPGOYFSPDLCMIKXVAOEGPTAFYKGFPSFLRLGSMNVVMFTYBOLK 300
XX
XX 301 LMKVQMLRESPP 312
XX |||||
XX 301 LMKVQMLRESPP 312
XX
XX RESULT 4
XX ID AAW88279 standard; protein; 312 AA.
XX
XX AAW88279;
XX
XX 12-APR-1999 (first entry)
XX
XX Human uncoupling protein 3 (UCP3).
XX
XX Uncoupling protein 3; UCP3; human; obesity; diabetes; hyperinsulinaemia;
XX hypermetabolism; therapy.
XX
XX Homo sapiens.

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XX MO9852958-A1.
XX 26-NOV-1998.
XX
XX 19-MAY-1998; 98MO-US010215.
XX
XX 20-MAY-1997; 97US-0047179P.
XX 08-AUG-1997; 97GB-00016886.
XX 09-DEC-1997; 97US-0069141P.
XX
XX (MERI) MERCK & CO INC.
XX
XX Liu Q, Chen F;
XX WPI; 1999-059737/05.
XX N-PSDB; AAV84254.
XX
XX New isolated human uncoupling protein 3 - used to identify compounds
XX which can modulate energy expenditure and body weight regulation, e.g. in
XX the treatment of obesity or diabetes.
XX
XX Claim 3; Page 58; 87p; English.
XX
XX This is human uncoupling protein 3 (UCP3), a novel protein that is
XX involved in energy expenditure and body weight regulation and whose
XX expression is mostly limited to skeletal muscle. The amino acid sequence
XX was deduced from the nucleotide sequence of an isolated foetal brain cDNA
XX clone (see AAV84254). The invention additionally provides related
XX recombinant expression vectors and recombinant host cells. UCP3
XX polypeptides and transformed recombinant cell lines can be used for
XX identifying modulators of UCP3 activity. The modulators can be used for
XX treating diseases such as obesity and diabetes, by manipulating the
XX interrelated processes of balancing food intake, energy expenditure and
XX glucose metabolism within the patient. They can also be used to treat
XX hyperactive conditions of energy expenditure which originate in the
XX mitochondria of skeletal muscle. UCP3 nucleic acids are useful in gene
XX therapy of obesity and obesity-related indications, including diabetes,
XX and of mitochondrial-associated hypermetabolism
XX
XX Sequence 312 AA;
XX
XX Query Match 100.0%; Score 1620; DB 2; Length 312;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-165;
XX Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MGLKPSDVPPTMAVVFGLGAGTACPADLVTPPLDTAKVRLQIGENQAVQTARLVQYRG 60
XX |||||
XX 1 MGLKPSDVPPTMAVVFGLGAGTACPADLVTPPLDTAKVRLQIGENQAVQTARLVQYRG 60
XX
XX 61 VGTGTLTWTRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPKGDNSLTTR 120
XX |||||
XX 61 VGTGTLTWTRTGPGSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPKGDNSLTTR 120
XX
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX |||||
XX 121 LAGCTTGAAVAVTCAOPTDVVKRFQASIHGSPRSRDKTSGTMDARTTAREGCVGLMK 180
XX
XX 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX |||||
XX 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPV 240
XX
XX 241 VKTRYNNSPPGOYFSPDLCMIKXVAOEGPTAFYKGFPSFLRLGSMNVVMFTYBOLK 300
XX |||||
XX 241 VKTRYNNSPPGOYFSPDLCMIKXVAOEGPTAFYKGFPSFLRLGSMNVVMFTYBOLK 300
XX
XX 301 LMKVQMLRESPP 312
XX |||||
XX 301 LMKVQMLRESPP 312
XX
XX RESULT 5
XX AAY31904

```

ID AAY31904 standard; protein; 312 AA.
 XX
 AC AAY31904;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Human uncoupling protein 3.
 XX
 KM Uncoupling protein 3; UCP3; human; obesity; diabetes; diagnosis;
 gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 70 /note= "substituted by Trp in C208T polymorphism"
 FT Misc-difference 102 /note= "substituted by Val in G304A polymorphism"
 FT Misc-difference 142 /note= "C-terminal residue in C427T polymorphism"
 FT
 XX W09948905-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 23-MAR-1999; 99WO-US006317.
 XX
 PR 23-MAR-1999; 98US-0078972P.
 XX
 PA (MUSC-) MUSC FOUND RES DEV.
 XX
 PI Garvey WT, Argypopoulos G;
 XX
 DR WPI; 1999-591072/50.
 DR N-PSDB; AA219969.
 XX
 PT Use of uncoupled protein 2 or 3 as markers for identifying subjects at
 PT risk of developing obesity or diabetes.
 XX
 PS Disclosure; Page 103-104; 112pp; English.
 XX
 CC The present sequence represents human uncoupling protein 3 (UCP3). The
 CC invention relates to the discovery that the presence of a single
 CC nucleotide polymorphism (SNP) in a nucleic acid encoding UCP3 (see
 CC AA219969) or UCP2 (see AA219968) can correlate with the development of
 CC obesity and type II diabetes mellitus. In UCP3, the SNP may generate a
 CC Trp for Arg substitution at position 70 of the encoded protein, a protein
 CC truncated after residue 142, or a Val for Ile substitution at position
 CC 102. Methods are provided for identifying a subject at risk of developing
 CC obesity and/or diabetes by detection of the SNP in the UCP2 UCP3 nucleic
 CC acid or amino acid sequence. An antibody to an antigen of the altered
 CC UCP2 can be used in such a method
 XX
 SQ Sequence 312 AA;
 Query Match 100.0%; Score 1620; DB 2; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2.2e-165; Indels 0; Gaps 0;
 Matches 312; Conservative 0; Mismatches 0;
 DB 1 MWGLKSDVPTMAVFLAGTAACFADLVTPPLDTAKRLQIQGENOVAQTARLVQYRG 60
 QY 1 VGLTILTWRTGPGSPYNGLVAGLOROMSPASIRIGLVDVQVYTPKGDNSSLTTRI 120
 DB 61 VGLTILTWRTGPGSPYNGLVAGLOROMSPASIRIGLVDVQVYTPKGDNSSLTTRI 120
 QY 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRKSGTMDAYRTIAREGVGLWK 180
 DB 121 LAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRKSGTMDAYRTIAREGVGLWK 180
 QY 181 GTLPNTMRNAIVNCAEVVTDILKEKLDYHLLTDNPFCHVSAFGAGFCATVVASPDV 240

DB 181 GTLPNTMRNAIVNCAEVVTDILKEKLDYHLLTDNPFCHVSAFGAGFCATVVASPDV 240
 QY 241 VKTRYNNSPPGOYFSPDLCMKVVAQSEGTAFYKGFPSFRLGSMNVMTVEQLRRA 300
 DB 241 VKTRYNNSPPGOYFSPDLCMKVVAQSEGTAFYKGFPSFRLGSMNVMTVEQLRRA 300
 QY 301 LMKVQMLRESPE 312
 DB 301 LMKVQMLRESPE 312
 RESULT 6
 ID AAY54600 standard; protein; 312 AA.
 XX
 AC AAY54600;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Amino acid sequence of a human uncoupling protein designated HHFCW60.
 XX
 KM Human; HHFCW60; mitochondrial uncoupling protein family; muscle wasting;
 uncoupling protein; wound; tissue repair; inflammation; cachexia.
 XX
 OS Homo sapiens.
 XX
 OS W0200002577-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 02-DEC-1998; 98WO-EP007802.
 XX
 PR 09-JUL-1998; 98GB-00014926.
 XX
 PA (SMIT) SMITHKLINE BEECHAM PLC.
 XX
 PI Clapham JC, Beeley LJ, Godden RJ;
 XX
 DR WPI; 2000-147542/13.
 DR N-PSDB; AA246055.
 XX
 PT Use of uncoupling protein, polynucleotide and compound activating it, in
 PT treating wounds, inflammation, tissue repair, muscle wasting, and
 PT cachexia.
 XX
 PS Claim 5; Page 22-23; 29pp; English.
 XX
 CC The present sequence represents a HHFCW60 polypeptide, which is a member
 CC of the mitochondrial uncoupling protein family. The HHFCW60
 CC polynucleotide has homology with human uncoupling protein 2. The
 CC polynucleotide sequence was isolated from a cDNA library derived from
 CC human skeletal muscle cell mRNA, and mRNA from the cell lines
 CC rhabdomyosarcoma, caaki, and SHSY 5Y. The protein is useful in producing
 CC antibodies and in screening for antagonist and agonist. The
 CC polynucleotide is useful as a reagent for diagnosing and determining
 CC susceptibility to the disease by detecting the mutation in the HHFCW60
 CC gene. The polynucleotide, protein, and antibodies against HHFCW60 are
 CC useful in screening for the compounds that have an effect on the
 CC production of mRNA and polypeptides in the cell. These compounds are used
 CC to treat wounds, tissue repair, inflammation, muscle wasting or cachexia
 XX
 SQ Sequence 312 AA;
 Query Match 100.0%; Score 1620; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2.2e-165; Indels 0; Gaps 0;
 Matches 312; Conservative 0; Mismatches 0;
 DB 1 MWGLKSDVPTMAVFLAGTAACFADLVTPPLDTAKRLQIQGENOVAQTARLVQYRG 60
 QY 1 VGLTILTWRTGPGSPYNGLVAGLOROMSPASIRIGLVDVQVYTPKGDNSSLTTRI 120

Db 61 VLGCTIIMVTEBPCSPYNGLVAGLORQMSFASIRIGLYDSVKQVYTPKGADNSLITRI 120
 Qy 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRKSGTMDARTIAREBGVGLMK 180
 Db 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRKSGTMDARTIAREBGVGLMK 180
 Qy 181 GLTPNIMRNAIVNCAEVVYTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPDV 240
 Db 181 GLTPNIMRNAIVNCAEVVYTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPDV 240
 Qy 241 VKTRYNNSPPGQYFSPDLCMIKVAOEGPTAFYKGTPTPSFLRLGSMNVVMFVTEBOLKRA 300
 Db 241 VKTRYNNSPPGQYFSPDLCMIKVAOEGPTAFYKGTPTPSFLRLGSMNVVMFVTEBOLKRA 300
 Qy 301 LMKVQMLRESPP 312
 Db 301 LMKVQMLRESPP 312

RESULT 7
 AAY44253
 ID AAY44253 standard; protein; 312 AA.
 XX
 AC AAY44253;

DT 28-FEB-2000 (first entry)
 DE Human mitochondrial anion carrier, uncoupling protein-3.
 XX

KM Mitochondrial uncoupling protein-3; UCP-3; mitochondrial anion carrier;
 KM MAC; modulator; transport protein; fatty acid anion; mitochondria;
 KM assay vesicle; metabolic disorder; diabetes; obesity; cancer; human.
 XX

OS Homo sapiens.
 XX
 PN WO964458-A1.
 XX

PD 16-DEC-1999.
 XX

PF 08-JUN-1999; 99WO-US012623.
 XX

PR 08-JUN-1998; 98US-00093662.
 XX

PA (UYBO-) UNIV BOSTON.
 XX

PI Corkey BE, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;
 XX

DR WPI; 2000-087200/07.
 XX

DR N-PSDB; AA229245.
 XX

PT Identifying modulators of mitochondrial anion carriers, potentially
 PT useful for treating metabolic disease, e.g. diabetes and obesity.
 XX

PS Claim 11; Page 73-74; 80pp; English.
 XX

CC The present sequence is a human uncoupling protein-3 (UCP-3) which is a
 CC mitochondrial anion carrier (MAC). The UCPs transport free fatty acid
 CC anions across the inner mitochondrial membrane to induce cyclical proton
 CC movement. This transport is tightly related to oxidation of fatty acids
 CC in the mitochondria, thereby converting fatty acids into energy rather
 CC than storing them. The uncoupling protein is used in the preparation of
 CC assay vesicles that are used to identify modulators of MAC activity. MAC
 CC modulators are useful for treating metabolic disorders, particularly
 CC diabetes and obesity. Modulators that act as inhibitors can be used to
 CC treat conditions requiring a reduction in energy expenditure, e.g. in
 CC cancer patients or the elderly
 XX

SQ Sequence 312 AA;
 XX

Query Match 100.0%; Score 1620; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2,2e-165;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLKPSDVPPTMAVFEIAGTAACPADLVTEPLDTAKVRLQIQENQAVQTAFLVQYRG 60
 Db 1 MGLKPSDVPPTMAVFEIAGTAACPADLVTEPLDTAKVRLQIQENQAVQTAFLVQYRG 60
 Qy 61 VLGCTIIMVTEBPCSPYNGLVAGLORQMSFASIRIGLYDSVKQVYTPKGADNSLITRI 120
 Db 61 VLGCTIIMVTEBPCSPYNGLVAGLORQMSFASIRIGLYDSVKQVYTPKGADNSLITRI 120
 Qy 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRKSGTMDARTIAREBGVGLMK 180
 Db 121 LAGCTTGAMAVTCAOPTDVVKRFPQASIHGSPRSRKSGTMDARTIAREBGVGLMK 180
 Qy 181 GLTPNIMRNAIVNCAEVVYTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPDV 240
 Db 181 GLTPNIMRNAIVNCAEVVYTDILKEKLDYHLTDNFPCHFVSAFGAGFCATVVASPDV 240
 Qy 241 VKTRYNNSPPGQYFSPDLCMIKVAOEGPTAFYKGTPTPSFLRLGSMNVVMFVTEBOLKRA 300
 Db 241 VKTRYNNSPPGQYFSPDLCMIKVAOEGPTAFYKGTPTPSFLRLGSMNVVMFVTEBOLKRA 300
 Qy 301 LMKVQMLRESPP 312
 Db 301 LMKVQMLRESPP 312

RESULT 8
 AAB74296
 ID AAB74296 standard; protein; 312 AA.
 XX

AC AAB74296;
 XX

DT 21-JUN-2001 (first entry)
 DE Human UCP3 protein.
 XX

KM UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus.
 KM
 XX

OS Homo sapiens.
 XX

PN WO200118232-A2.
 XX

PD 15-MAR-2001.
 XX

PF 08-SEP-2000; 2000MO-US024784.
 XX

PR 08-SEP-1999; 99US-0152789P.
 XX

PA (GENA-) GENAISSANCE PHARM INC.
 XX

PA (STEP/) STEPHENS J C.
 XX

PI Chew A, Choi JY, Denton RR, Nandabalan K;
 XX

DR WPI; 2001-218562/22.
 XX

PT Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
 PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
 PT useful for the design of drugs for treating obesity.
 XX

PS Claim 10; Fig 6; 94pp; English.
 XX

CC The present invention relates to the human uncoupling protein 3
 CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
 CC polymorphisms are associated with obesity, especially diabetes mellitus
 CC associated obesity. They polymorphisms may be identified and analysed to
 CC determine whether an individual is susceptible to obesity and may be used
 CC as the basis for targeted design of drugs to treat obesity. The present
 CC sequence is UCP3 protein
 XX

SQ Sequence 312 AA;
 XX

Query Match 100.0%; Score 1620; DB 4; Length 312;
 Best Local Similarity 100.0%; Pred. No. 2,2e-165;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  MVGLKPSDVPPTMAVKFLGAGTAACFADLVTEPPLDTAKVRLQIQENQAVQTARLVQYRG 60
DB      1  MVGLKPSDVPPTMAVKFLGAGTAACFADLVTEPPLDTAKVRLQIQENQAVQTARLVQYRG 60
QY      61  VLGTLTIVWRTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKGDNSLTTTRI 120
DB      61  VLGTLTIVWRTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKGDNSLTTTRI 120
QY      121  LAGCTTGMAATVCAOPTDVVVRFOASIHLPSSDRKYSGMTDAVRTIAREEGVRLMK 180
DB      121  LAGCTTGMAATVCAOPTDVVVRFOASIHLPSSDRKYSGMTDAVRTIAREEGVRLMK 180
QY      181  GTLPINMNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFAGFCATVVASPYDV 240
DB      181  GTLPINMNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFAGFCATVVASPYDV 240
QY      241  VKTRYMNSPPGQYSPFLDCMIMVAOEGPTAFYKGFPTPSFLRSGMNVMMVPTVYEQLKRA 300
DB      241  VKTRYMNSPPGQYSPFLDCMIMVAOEGPTAFYKGFPTPSFLRSGMNVMMVPTVYEQLKRA 300
QY      301  LMKVQMLRESPP 312
DB      301  LMKVQMLRESPP 312

```

RESULT 9

AAE04298

ID AAE04298 standard; protein; 312 AA.

AAE04298;

04-SEP-2001 (first entry)

Human uncoupling protein-3 (UCP3).

Human; UCP3; uncoupling protein-3; chromosome 11q13; gene therapy;

atherosclerosis; hypercholesterolaemia; antilipemic.

Homo sapiens.

WO200143760-A2.

21-JUN-2001.

18-DEC-2000; 2000WO-BP012931.

17-DEC-1999; 99GB-00030100.

(SMK) SMITHKLINE BEECHAM PLC.

Clapham JC;

WPI; 2001-398073/42.

N-PSDB; AAD08530.

Use of a compound selected from UCP3 polypeptide, a compound which activates the polypeptide, or a polynucleotide encoding the polypeptide, for treating atherosclerosis or hypercholesterolaemia.

Claim 5; Page 19; 24pp; English.

The present sequence is human UCP3 (uncoupling protein-3) protein. UCP3 gene is located in chromosome 11q13. UCP3 protein and polynucleotides encoding them are useful for identifying agonist compounds which are potentially useful in therapy. UCP3 protein is useful for inducing an immunological response, as immunogen to produce antibodies immunospecific for UCP3 protein, and in a method for the structure-based design of an agonist of UCP3 protein. UCP3 sequences are useful to configure screening methods for detecting the effect of added components on the production of cRNA and polypeptide in cells. UCP3 DNA is used in gene therapy. A compound which activates UCP3 protein or a polynucleotide encoding UCP3 protein are used for the manufacture of medicament for treating

CC atherosclerosis or hypercholesterolaemia
XX
SQ Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 2,2e-165;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  MVGLKPSDVPPTMAVKFLGAGTAACFADLVTEPPLDTAKVRLQIQENQAVQTARLVQYRG 60
DB      1  MVGLKPSDVPPTMAVKFLGAGTAACFADLVTEPPLDTAKVRLQIQENQAVQTARLVQYRG 60
QY      61  VLGTLTIVWRTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKGDNSLTTTRI 120
DB      61  VLGTLTIVWRTEGPCSPYNGLVAGLQROMSFASIRIGLYDSVKQYVTPKGDNSLTTTRI 120
QY      121  LAGCTTGMAATVCAOPTDVVVRFOASIHLPSSDRKYSGMTDAVRTIAREEGVRLMK 180
DB      121  LAGCTTGMAATVCAOPTDVVVRFOASIHLPSSDRKYSGMTDAVRTIAREEGVRLMK 180
QY      181  GTLPINMNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFAGFCATVVASPYDV 240
DB      181  GTLPINMNAIVNCAEVVYTDILKEKLDYHLTDNPFCHVSAFAGFCATVVASPYDV 240
QY      241  VKTRYMNSPPGQYSPFLDCMIMVAOEGPTAFYKGFPTPSFLRSGMNVMMVPTVYEQLKRA 300
DB      241  VKTRYMNSPPGQYSPFLDCMIMVAOEGPTAFYKGFPTPSFLRSGMNVMMVPTVYEQLKRA 300
QY      301  LMKVQMLRESPP 312
DB      301  LMKVQMLRESPP 312

```

RESULT 10

AAB68050

ID AAB68050 standard; protein; 312 AA.

AAB68050;

29-JUN-2001 (first entry)

Amino acid sequence of a human uncoupling protein 3 (UCP3).

Uncoupling protein 3; UCP3; transgenic rodent; UCP3-related disease;

obesity; diabetes; hyperlipidemia; body weight disorder; wound healing;

cachexia; inflammation; tissue repair; atherosclerosis.

Homo sapiens.

WO200124625-A1.

12-APR-2001.

29-SEP-2000; 2000WO-GB003747.

01-OCT-1999; 99GB-00023334.

(SMK) SMITHKLINE BEECHAM PLC.

Abuin A; Clapham J;

WPI; 2001-273534/28.

N-PSDB; AAF84745.

New transgenic rodent, useful for determining phenotypic effect of a compound, comprises a polynucleotide encoding a human uncoupling protein 3 under control of regulatory sequence in its genome.

Disclosure; Page 24-25; 28pp; English.

The present sequence represents a human uncoupling protein 3 (UCP3). The UCP3 polynucleotide is used to produce a transgenic rodent comprising a UCP3 polynucleotide in its genome, under the control of a regulatory

CC sequence facilitating the expression of the polypeptide. The transgenic
 CC rodent is useful for determining the phenotypic effect of a compound,
 CC which may be used for treating UCP3-related disease such as obesity,
 CC diabetes, hyperlipidemia, body weight disorders, wound healing, cachexia,
 CC inflammation and tissue repair of atherosclerosis. The transgenic mice
 CC expressing human UCP3 have significantly reduced body weight compared to
 CC age-matched wild-type controls despite showing increased food intake,
 CC and thus are suitable for studies of body weight disorders, diabetes,
 CC obesity and inflammation and the evaluation of compounds that have
 CC potential to treat such diseases and disorders. The transgenic rodents
 CC are also useful for validation of the polypeptide expressed from the
 CC transgene as a drug target in addition to elucidating the function of a
 CC gene of interest. The transgenic rodents can also be used to test the
 CC efficacy of drug and drug administration regime for treating the above
 CC mentioned disorders and to investigate the effects of various drug
 CC treatments on the course of the disease

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 4; Length 312;

Best Local Similarity 100.0%; Pred. No. 2, 2e-165; Mismatches 0; Indels 0; Gaps 0;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQAVQTALVQYRG 60
 DB 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQAVQTALVQYRG 60
 QY 61 VLGTLLTMVTEGSPSPYNGLVAGLQROMSPASIRIGLYSVKQVYTPKADNSLTTTRI 120
 DB 61 VLGTLLTMVTEGSPSPYNGLVAGLQROMSPASIRIGLYSVKQVYTPKADNSLTTTRI 120
 QY 121 LAGCTGAMAVTCAOPTDVVKVRFQASIHGSPSRDKYSGTMDAYTTIAREBVGRLMK 180
 DB 121 LAGCTGAMAVTCAOPTDVVKVRFQASIHGSPSRDKYSGTMDAYTTIAREBVGRLMK 180
 QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDFNPFCHFVSAFGAGFCATVVASPDV 240
 DB 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDFNPFCHFVSAFGAGFCATVVASPDV 240
 QY 241 VKTRRNNSPPGOYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300
 DB 241 VKTRRNNSPPGOYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300
 QY 301 LMKVQMLRESPPF 312
 DB 301 LMKVQMLRESPPF 312

RESULT 11
 ABB81610
 ID ABB81610 standard; protein; 312 AA.

XX ABB81610;

XX 20-SEP-2002 (first entry)

XX UCP3L protein sequence.

XX UCP3L, UCP3s, diabetes, obesity, diabetic related condition; GKR;
 XX gene therapy; antidiabetic; anorectic; cardiatic; nephrotropic; GK;
 XX antilipase; blood glucose; glucokinase regulatory protein; liver;
 XX glucokinase; hepatic triglyceride accumulation; fibrinogen; HDL;
 XX hepatic fatty acid oxidation; high density lipoprotein; cholesterol;
 XX glucose; gestational diabetes; hyperglycaemic related disorder;
 XX kidney related disorder; cardiovascular disorder.

XX Undifferentiated.

XX US2002065239-A1.

XX 30-MAY-2002.

XX 14-MAR-2001; 2001US-00808457.

XX 15-MAR-2000; 2000US-0266328P.

XX (CAPL/) CAPLAN S L.
 XX (BOET/) BOETTCHER B R.
 XX (SLOS/) SLOSBERG E D.
 XX (CONN/) CONNELLY S.
 XX (KALE/) KALEKO M.
 XX (DESA/) DESAI U J.

XX Caplan SL, Boettcher BR, Slosberg ED, Connelly S, Kaleko M,
 XX Desai UJ

XX WPI, 2002-556735/59.
 XX N-PSDB; ABQ72999.

PT Treating condition related to elevated blood glucose levels, especially
 PT diabetes or obesity, involves administering polynucleotide sequence
 PT encoding glucokinase regulatory protein, to a subject.

PS Disclosure; Page 16-17; 42pp; English.

CC The present invention describes a method (M1) for treating a condition
 CC related to elevated blood glucose levels, which involves administering a
 CC polynucleotide sequence encoding a glucokinase regulatory protein (GKR),
 CC to a subject. Also described: (1) increasing liver glucokinase (GK)
 CC activity, by administering a polynucleotide sequence encoding GKR; and
 CC (2) a method (M2) treating diabetes or diabetes-related condition, by
 CC administering to a subject, one or more metabolism modifying proteins and
 CC peptides in combination with GK or GKR, or their combination (M1) and
 CC (M2) can be used for treating diabetes (type I and II diabetes) or
 CC diabetes-related conditions such as obesity, increased hepatic
 CC triglyceride accumulation, reduced hepatic fatty acid oxidation,
 CC increased fibrinogen levels, decreased apo A-I levels, decreased high
 CC density lipoprotein (HDL) cholesterol levels and decreased hepatic
 CC glucose utilization. The methods are also useful for treating gestational
 CC diabetes, hyperglycaemic related disorders such as increased cholesterol,
 CC kidney related disorders and cardiovascular disorders. The methods
 CC overcome a limitation to the over-expression of GK in the liver which
 CC usually increases liver size and hepatic fat accumulation in normal and
 CC diabetic mice. The present sequence represents a UCP3L protein which is
 CC given in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 100.0%; Score 1620; DB 5; Length 312;

Best Local Similarity 100.0%; Pred. No. 2, 2e-165; Mismatches 0; Indels 0; Gaps 0;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQAVQTALVQYRG 60
 DB 1 MVLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQAVQTALVQYRG 60
 QY 61 VLGTLLTMVTEGSPSPYNGLVAGLQROMSPASIRIGLYSVKQVYTPKADNSLTTTRI 120
 DB 61 VLGTLLTMVTEGSPSPYNGLVAGLQROMSPASIRIGLYSVKQVYTPKADNSLTTTRI 120
 QY 121 LAGCTGAMAVTCAOPTDVVKVRFQASIHGSPSRDKYSGTMDAYTTIAREBVGRLMK 180
 DB 121 LAGCTGAMAVTCAOPTDVVKVRFQASIHGSPSRDKYSGTMDAYTTIAREBVGRLMK 180
 QY 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDFNPFCHFVSAFGAGFCATVVASPDV 240
 DB 181 GTLPNIRNAIVNCAEVVYDILKEKLDYHLTDFNPFCHFVSAFGAGFCATVVASPDV 240
 QY 241 VKTRRNNSPPGOYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300
 DB 241 VKTRRNNSPPGOYFSPIDCMIKWVAOEGPTAFYKGFPSFLRLGSMVWVVFYEQLKRA 300
 QY 301 LMKVQMLRESPPF 312
 DB 301 LMKVQMLRESPPF 312

RESULT 12
AAE19348
ID AAE19348 standard; protein; 312 AA.
XX
AC AAE19348;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human mitochondrial uncoupling protein 3 (UCP3).
XX
KW Human; mitochondrial uncoupling protein 3; UCP3; obesity; diabetes;
XX body weight disorder; gene therapy; chromosome 11q13.
XX
OS Homo sapiens.
XX
PN WO200207754-A2.
XX
PD 31-JAN-2002.
XX
PF 25-JUL-2001; 2001WO-GE003341.
XX
PR 25-JUL-2000; 2000GB-00018248.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Clapham J;
XX
DR WPI; 2002-217023/27.
XX N-PSDB; AAD30499.
XX
PT Use of mitochondrial uncoupling protein 3 polypeptide, polynucleotide and
XX compounds which activate the polypeptide or polynucleotide for treating
XX obesity, diabetes or body weight disorder.
XX
PS Claim 5; Page 18; 22pp; English.
XX
CC The present sequence is human mitochondrial uncoupling protein 3 (UCP3).
XX The UCP3 gene is located on chromosome 11q13. UCP3 sequences are used for
XX identifying compounds which modulate their activity. They are used for
XX the manufacture of a medicament for treating obesity, diabetes and body
XX weight disorder. UCP3 sequences are also used in gene therapy
XX
SQ Sequence 312 AA;
Query Match 100.0%; Score 1620; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-165;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLGKSDVPPPTMAVKRLGAGTACFPADLVTFFPLDTAKVRLQIGENQAVQTARLVQYRG 60
DB 1 MVLGKSDVPPPTMAVKRLGAGTACFPADLVTFFPLDTAKVRLQIGENQAVQTARLVQYRG 60
QY 61 VLGTILTMVTEGCPSPYNGVAGLGRQMSFASIRIGLYDSVKQVTPKGDNSSLTTRI 120
DB 61 VLGTILTMVTEGCPSPYNGVAGLGRQMSFASIRIGLYDSVKQVTPKGDNSSLTTRI 120
QY 121 LAGCTTGAMAVTCAQPTDVVKVRPQASIHGSPSSDRKSGTMDAYTITAREEGVRLMK 180
DB 121 LAGCTTGAMAVTCAQPTDVVKVRPQASIHGSPSSDRKSGTMDAYTITAREEGVRLMK 180
QY 181 GTLPNIRNAINVCAEVVTTDLLEKLLDHLTDNPFCHVSAFGAGFCATVVASPVDV 240
DB 181 GTLPNIRNAINVCAEVVTTDLLEKLLDHLTDNPFCHVSAFGAGFCATVVASPVDV 240
QY 241 VKTRVNSPPGOVSPDLCMIKWAQSGPTAFYKGFPSFLRLGSMNVVWFVTEQLKRA 300
DB 241 VKTRVNSPPGOVSPDLCMIKWAQSGPTAFYKGFPSFLRLGSMNVVWFVTEQLKRA 300
QY 301 LMKVQMLRESPP 312
DB 301 LMKVQMLRESPP 312

RESULT 13
ADE54391
ID ADE54391 standard; protein; 312 AA.
XX
AC ADE54391;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P55916, SEQ ID NO 194.
XX
KW Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SN1; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
XX
DR GENBANK; P55916.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
XX injury (CCI) and spared nerve injury (SN1) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX the sequence data for this patent did not form part of the printed
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 312 AA;
Query Match 100.0%; Score 1620; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.2e-165;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPDLTAKVRLQIOGENQAVQTARLVQYRG 60
 Db 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPDLTAKVRLQIOGENQAVQTARLVQYRG 60
 QY 61 VLGITLITWRTGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYVTPPKGADNSLITRI 120
 Db 61 VLGITLITWRTGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYVTPPKGADNSLITRI 120
 QY 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHILGSPSRDKYSGTMDAYRTIAREBGVGLWK 180
 Db 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHILGSPSRDKYSGTMDAYRTIAREBGVGLWK 180
 QY 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPVVY 240
 Db 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPVVY 240
 QY 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGTPTSPFLRIGSNVVMFVYYEOLKRA 300
 Db 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGTPTSPFLRIGSNVVMFVYYEOLKRA 300
 QY 301 LMKVQMLRESPE 312
 Db 301 LMKVQMLRESPE 312

RESULT 14
 AAWB1587
 ID AAWB1587 standard; protein; 312 AA.
 AC AAWB1587;
 DT 09-FEB-1999 (first entry)
 DE Human uncoupling protein 3 (UCP3).
 KW Uncoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;
 KW protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;
 KW HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;
 KW non-insulin dependent diabetes mellitus; diagnosis; human.
 OS Homo sapiens.
 PN MO9845438-A1.
 PD 15-OCT-1998.
 PF 08-APR-1998; 98WO-US006959.
 PR 09-APR-1997; 97US-0043447P.
 PR 12-MAY-1997; 97US-0046254P.
 PR 15-JUL-1997; 97US-00892745.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PI Lowell BB, Flier JS;
 DR WPI, 1998-594483/50.
 DR N-PSDB; AAV71710.
 PT New isolated uncoupling protein, UCP-3 - used to develop products for
 PT modulating thermogenesis in tissues, e.g. for treating obesity or muscle
 PT wasting caused by infection or cancer.
 PS Claim 5; Fig 1A-C; 98pp; English.
 XX This represents a human uncoupling protein 3 (UCP3). A host cell
 XX transformed with a construct comprising the UCP3 nucleic acid can be used
 XX for the recombinant production of the protein. The UCP3 is involved in
 XX the regulation of thermogenesis in mammals. The nucleic acids (AAV71710
 XX to AAV71712) can be used for identifying compounds which alter UCP3
 XX activity. Enhancers of UCP3 can be used for enhancing protein catabolism
 XX in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can

CC be used for inhibiting protein catabolism in a mammal such as inhibiting
 CC muscle wasting. They can be used for curtailing muscle wasting due to
 CC infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.
 CC muscular dystrophy) or as a possible treatment for non-insulin dependent
 CC diabetes mellitus. The products can also be used for detection and
 CC diagnosis
 XX
 SQ Sequence 312 AA;
 Query Match 99.8%; Score 1616; DB 2; Length 312;
 Best Local Similarity 99.7%; Pred. No. 5.9e-165;
 Matches 311; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPDLTAKVRLQIOGENQAVQTARLVQYRG 60
 Db 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTPPDLTAKVRLQIOGENQAVQTARLVQYRG 60
 QY 61 VLGITLITWRTGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYVTPPKGADNSLITRI 120
 Db 61 VLGITLITWRTGSPSPYNGLVAGLQROMSPASIRIGLYDSVKQYVTPPKGADNSLITRI 120
 QY 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHILGSPSRDKYSGTMDAYRTIAREBGVGLWK 180
 Db 121 LAGCTTGAMAATCAOPTDVVKVRFQASIHILGSPSRDKYSGTMDAYRTIAREBGVGLWK 180
 QY 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPVVY 240
 Db 181 GTLPNIMRNAIVNCAEVVYTDILKEKLDYHLITDNFPCHFVSAFAGFCATVVASPVVY 240
 QY 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGTPTSPFLRIGSNVVMFVYYEOLKRA 300
 Db 241 VKTRYNNSPPGOYFSPFLDCMIRKVAOEGPTAFYKGTPTSPFLRIGSNVVMFVYYEOLKRA 300
 QY 301 LMKVQMLRESPE 312
 Db 301 LMKVQMLRESPE 312

RESULT 15
 AAWB1588
 ID AAWB1588 standard; protein; 403 AA.
 AC AAWB1588;
 DT 09-FEB-1999 (first entry)
 DE Protein encoded by human UCP3 gene reading frame 1.
 KW Uncoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;
 KW protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;
 KW HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;
 KW non-insulin dependent diabetes mellitus; diagnosis; human.
 OS Homo sapiens.
 PN MO9845438-A1.
 PD 15-OCT-1998.
 PF 08-APR-1998; 98WO-US006959.
 PR 09-APR-1997; 97US-0043447P.
 PR 12-MAY-1997; 97US-0046254P.
 PR 15-JUL-1997; 97US-00892745.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PI Lowell BB, Flier JS;
 DR WPI, 1998-594483/50.
 DR N-PSDB; AAV71710.
 PT New isolated uncoupling protein, UCP-3 - used to develop products for
 PT modulating thermogenesis in tissues, e.g. for treating obesity or muscle
 PT wasting caused by infection or cancer.
 PS Claim 5; Fig 1A-C; 98pp; English.
 XX This represents a human uncoupling protein 3 (UCP3). A host cell
 XX transformed with a construct comprising the UCP3 nucleic acid can be used
 XX for the recombinant production of the protein. The UCP3 is involved in
 XX the regulation of thermogenesis in mammals. The nucleic acids (AAV71710
 XX to AAV71712) can be used for identifying compounds which alter UCP3
 XX activity. Enhancers of UCP3 can be used for enhancing protein catabolism
 XX in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can

XX MPI. 1998-594483/50.
DR N-ESDB; AAV71710.

XX New isolated uncoupling protein, UCP-3 - used to develop products for
PT modulating thermogenesis in tissues, e.g. for treating obesity or muscle
PT wasting caused by infection or cancer.

XX Disclosure; Fig 1A-C; 98pp; English.

XX Sequences AAW81588 to AAW81590 represent protein fragments encoded by the
CC three reading frames of the human uncoupling protein 3 (UCP3) gene. The
CC invention provides human and mouse UCP3 genes (AAV71710 and AAV71712)
CC encoding UCP3 proteins (AAW81587 and AAW81595) respectively. A host cell
CC transformed with a construct comprising the UCP3 nucleic acid can be used
CC for the recombinant production of the protein. The UCP3 is involved in
CC the regulation of thermogenesis in mammals. The nucleic acids (AAV71710
CC to AAV71712) can be used for identifying compounds which alter UCP3
CC activity. Enhancers of UCP3 can be used for enhancing protein catabolism
CC in a mammal and can be used as anti-obesity drugs. Inhibitors of UCP3 can
CC be used for inhibiting protein catabolism in a mammal such as inhibiting
CC muscle wasting. They can be used for curtailing muscle wasting due to
CC infection (e.g. HIV), cancer, tumour cachexia, muscle diseases (e.g.
CC muscular dystrophy) or as a possible treatment for non-insulin dependent
CC diabetes mellitus. The products can also be used for detection and
CC diagnosis

XX SQ Sequence 403 AA;

Query Match 99.4%; Score 1610; DB 2; Length 403;

Best Local Similarity 99.4%; Pred. No. 3 8e-164;

Matches 310; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVLKPSDVPPTMAVYKFGAGTACPRADLVTFPLDTAKYRLQIQENQAVQTARLVQYRG 60
DB 60 MVLKPSDVPPTMAVYKFGAGTACPRADLVTFPLDTAKYRLQIQENQAVQTARLVQYRG 119
QY 61 VLGTLITWRTREGSPYNGVAGLOROMSFASIRIGLYDSVKOYVTPKGADNSLTTRI 120
DB 120 VLGTLITWRTREGSPYNGVAGLOROMSFASIRIGLYDSVKOYVTPKGADNSLTTRI 179
QY 121 IAGCTTGAMAAYTCAOPTDVVKVRFQASIHGSPRSRDKYSGTMDAYRTIAREEGVGLMK 180
DB 180 IAGCTTGAMAAYTCAOPTDVVKVRFQASIHGSPRSRDKYSGTMDAYRTIAREEGVGLMK 239
QY 181 GTLPNIMRNNAIVNCAEVVYDILKEKLDYHLITDNFCHYVSAFGAGFCATVVASPDV 240
DB 240 GTLPNIMRNNAIVNCAEVVYDILKEKLDYHLITDNFCHYVSAFGAGFCATVVASPDV 299
QY 241 VETRTMNSPFGQYFSPPLDMIMVNAOEGPTAFYKGFPSFLRIGSMNVVMFVTEQLKRA 300
DB 300 VETRTMNSPFGQYFSPPLDMIMVNAOEGPTAFYKGFPSFLRIGSMNVVMFVTEQLKRA 359
QY 301 LMKVOMLRSPF 312
DB 360 LMKVOMLRSPF 371

Search completed: May 17, 2004, 11:51:55
Job time : 61 secs

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OM protein - protein search, using SW model

Run on: May 17, 2004, 11:49:46 ; Search time 20 Seconds
(without alignments)
1500.588 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620
Sequence: 1 MVLKPSDVPPTMAVKFLGA.....TYEQLKALMKVQLRESPP 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1620 | 100.0 | 312 | 2 JC5522 | uncoupling protein |
| 2 | 910.5 | 56.2 | 307 | 2 G01858 | uncoupling protein |
| 3 | 905 | 55.9 | 306 | 2 A32446 | uncoupling protein |
| 4 | 903.5 | 55.8 | 307 | 2 A26294 | uncoupling protein |
| 5 | 885.5 | 54.7 | 306 | 2 A31106 | mitochondrial unco |
| 6 | 873.5 | 53.9 | 307 | 2 S34268 | uncoupling protein |
| 7 | 846 | 52.2 | 288 | 2 S03603 | uncoupling protein |
| 8 | 687 | 42.4 | 306 | 2 T07793 | uncoupling protein |
| 9 | 682 | 42.1 | 306 | 2 T47570 | uncoupling protein |
| 10 | 673 | 41.5 | 306 | 2 T52024 | uncoupling protein |
| 11 | 524 | 32.3 | 325 | 2 JC7553 | brain mitochondria |
| 12 | 500.5 | 30.9 | 313 | 2 T05577 | uncoupling protein |
| 13 | 478.5 | 29.5 | 305 | 2 H86274 | F7A19.22 protein - |
| 14 | 472.5 | 29.2 | 313 | 2 D84613 | hypothetical prote |
| 15 | 439 | 27.1 | 343 | 2 T15253 | hypothetical prote |
| 16 | 432 | 26.7 | 314 | 2 A36305 | 2-oxoglutarate/mal |
| 17 | 427 | 26.4 | 323 | 2 T25459 | hypothetical prote |
| 18 | 426 | 26.3 | 314 | 2 A56650 | 2-oxoglutarate car |
| 19 | 386.5 | 23.9 | 282 | 2 T49628 | probable dicarboxy |
| 20 | 373 | 23.0 | 280 | 2 S44091 | oxoglutarate/malat |
| 21 | 364.5 | 22.5 | 288 | 2 S51351 | hypothetical prote |
| 22 | 327.5 | 20.2 | 324 | 2 S25357 | mitochondrial unco |
| 23 | 318 | 19.6 | 302 | 2 S65040 | 2-oxoglutarate/mal |
| 24 | 310 | 19.1 | 297 | 2 T07405 | oxoglutarate/malat |
| 25 | 309 | 18.5 | 302 | 2 S65042 | probable 2-oxoglut |
| 26 | 299.5 | 18.1 | 331 | 2 T51899 | probable carrier p |
| 27 | 293 | 17.9 | 322 | 2 S57116 | probable oxalacet |
| 28 | 289.5 | 16.8 | 311 | 2 T37603 | tricarboxylate tra |
| 29 | 272.5 | 16.8 | 311 | 2 A46595 | |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 268 | 16.5 | 93 | 2 S16082 | uncoupling protein |
| 31 | 267.5 | 16.5 | 309 | 2 T48156 | hypothetical prote |
| 32 | 267 | 16.5 | 298 | 2 B43646 | ADP,ATP carrier pr |
| 33 | 265 | 16.4 | 298 | 1 S03894 | ADP,ATP carrier pr |
| 34 | 258 | 15.9 | 298 | 1 XWBO | ADP,ATP carrier pr |
| 35 | 258 | 15.9 | 358 | 2 T09109 | envelope protein L |
| 36 | 257 | 15.9 | 298 | 2 S37210 | ADP,ATP carrier pr |
| 37 | 256.5 | 15.8 | 373 | 2 S48451 | probable membrane |
| 38 | 253.5 | 15.6 | 311 | 2 G01789 | citrate transpor |
| 39 | 252.5 | 15.6 | 339 | 2 A41677 | ADP,ATP carrier pr |
| 40 | 252 | 15.6 | 298 | 2 T60173 | adenine nucleotide |
| 41 | 252 | 15.6 | 355 | 2 T09110 | envelope protein L |
| 42 | 251 | 15.5 | 301 | 2 S51132 | ADP,ATP carrier pr |
| 43 | 250 | 15.4 | 298 | 2 S31814 | ADP,ATP carrier pr |
| 44 | 249.5 | 15.4 | 318 | 1 A31978 | ADP,ATP carrier pr |
| 45 | 249 | 15.4 | 352 | 2 T01729 | mitochondrial solu |

ALIGNMENTS

RESULT 1

JC5522

uncoupling protein UCP3, mitochondrial - human
C/Species: Homo sapiens (man)

C/Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 21-Jan-2000
C/Accession: JC5522

R/Vidal-Puig, A.; Solanes, G.; Grujic, D.; Flier, J.S.; Lowell, B.B.

Biochem. Biophys. Res. Commun. 235, 79-82, 1997

A/Title: UCP3: An uncoupling protein homologue expressed preferentially and abundantly i

A/Reference number: JC5522; MUID:9739440; PMID:9196039

A/Accession: JC5522

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-312 <VID>

A/Cross-references: DDBJ:AF001787; NID:G2198812; PIDN:AA051369.1; PID:G2198813

A/Experimental source: skeletal muscle

A/Comment: This protein is an inner mitochondrial membrane transporter which dissipates

C/Genetics:

A/Gene: GDB:UCP3

A/Cross-references: GDB:6278985

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C/Keywords: mitochondrion

F/10-106/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F/113-207/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F/214-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1620; DB 2; Length 312;

Best local similarity 100.0%; Pred. No. 2.6e-14;

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIQENQAVQTRLVQYRG | 60 |
| DB | 1 | MVLKPSDVPPTMAVKFLGAGTAACFADLVTPPLDTAKVRLQIQENQAVQTRLVQYRG | 60 |
| QY | 61 | VLGTLITLWRTGSPSPYNGVLVAGLQRMSPASIRIGLYDSVQVYTPKGADNSLTTRI | 120 |
| DB | 61 | VLGTLITLWRTGSPSPYNGVLVAGLQRMSPASIRIGLYDSVQVYTPKGADNSLTTRI | 120 |
| QY | 121 | LAGCTTGAMAVTCAQPTDVVYKVPQASIHGSPRSRKISGTMADYRTTAREGTVGLWK | 180 |
| DB | 121 | LAGCTTGAMAVTCAQPTDVVYKVPQASIHGSPRSRKISGTMADYRTTAREGTVGLWK | 180 |
| QY | 181 | GTLPMTRMAIVNCAVVTYDIKELLDYHLITDNPCHFVSAPGAFATVVASPVV | 240 |
| DB | 181 | GTLPMTRMAIVNCAVVTYDIKELLDYHLITDNPCHFVSAPGAFATVVASPVV | 240 |
| QY | 241 | VKTRVNSPPGOYFSPDLQMKIKVNAQEGPTAFYKGTPTPFLRLGNNVVFVTEQLKKA | 300 |
| DB | 241 | VKTRVNSPPGOYFSPDLQMKIKVNAQEGPTAFYKGTPTPFLRLGNNVVFVTEQLKKA | 300 |
| QY | 301 | LKRVQMLRESPP 312 | |
| | | | |

DB 301 LMKVLMRESPP 312

RESULT 2
G01858
uncoupling protein 1, mitochondrial - human

N.Alternate names: UCP1
C.Species: Homo sapiens (man)
C.Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 20-Jun-2000
C.Accession: G01858; S78473; S29141; A60793; A45763
R.Bouillaud, F.
submitted to the EMBL Data Library, June 1995

A.Reference number: G08642

A.Accession: G01858
A.Status: translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-307 <BOU>
A.Cross-references: EMBL:U28480; NID:g1155218; PIDN:AAA05271.1; PID:g1155219

A.Accession: S78473
A.Molecule type: DNA

A.Residues: 1-20, 'P', '22-307 <BOU>
A.Cross-references: EMBL:X51952; NID:g37606; PIDN:CAA36214.1; PID:g1177311

R.Cassard, A.M.; Bouillaud, F.; Mattei, M.G.; Hentz, E.; Raimbault, S.; Thomas, M.; Ricq
J. Cell. Biochem. 43, 255-264, 1990

A.Title: Human uncoupling protein gene: structure, comparison with rat gene, and assignm
A.Reference number: A45763; MUID:90338166; PMID:2380264

A.Accession: S29141
A.Molecule type: DNA

A.Residues: 1-20, 'P', '22-108', 'SK', '111,113-133', 'S', '135-197', 'T', '199-216', 'L', '218-307 <CAS>
A.Cross-references: EMBL:X51952; NID:g37606; PIDN:CAA36214.1

R.Bouillaud, F.; Villarroya, F.; Hentz, E.; Raimbault, S.; Cassard, A.M.; Ricquier, D.
Clin. Sci. 75, 21-27, 1988

A.Title: Detection of brown adipose tissue uncoupling protein mRNA in adult patients by
A.Reference number: A60793; MUID:88311701; PMID:3165741

A.Accession: A60793
A.Status: not compared with conceptual translation

A.Molecule type: DNA
A.Residues: 193-133, 'S', '135-196 <BOU>
C.Comment: This protein is responsible for the generation of heat by brown fat.

C.Genetics:
A.Gene: GDB:UCP1; UCP

A.Cross-references: GDB:128179; OMIM:113730

A.Map position: 4q31-4q31

A.Introns: 42/3; 109/1; 176/1; 210/1; 270/2
C.Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C.Keywords: adipose tissue; duplication; mitochondrion; transmembrane protein
F.10-103/Domain: ADP,ATP carrier protein repeat homology <ACPI>
F.110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F.209-296/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 56.2%; Score 910.5; DB 2; Length 307;
Best Local Similarity 58.7%; Pred. No. 5.1e-76;
Matches 178; Conservative 47; Mismatches 73; Indels 5; Gaps 2;

DB 1 MVLKSDVPPPTMAVVFLLAGTAAACFADLVTPPLDTAKVRLIOGQENQAVQARLVOYRG 60
1 MGLTASDVHPTLGLVQLFSAGIACADLVITPPLDTAKVRLVOQS--CPTSSVIRYKG 57
DB 1 VGTGTLTWRTEGPCSPYNGLVAGLQROWSPASIRIGLYDSVKQYTPKGDNSLITRI 120
61 VGTGTLTWRTEGPCSPYNGLVAGLQROWSPASIRIGLYDSVKQYTPKGDNSLITRI 120
DB 58 VLGTTTAAVKTBERMGLKSGLPAGLQROISASLRIGLVDTVQEFITAGETAPSLGSKI 117
121 LAGCTTGAAVTCAGPTDVVKVRFQASIHGSPRSRKYSGTMDAYRTTAREGVRLGK 180
118 LAGLTGGVAVFICGPTLVKVRLLQASHLGLKIP--RYGTGNAYRIIATTEGLTGLWK 175
DB 181 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTNPFCHEFVSAGFCATVVASPVY 240
176 GTLPNIMRNATVNCAGVVTYDILKEKLPVKNLADVDVPCHLISALIAFCATVVASPVY 235
DB 241 VKTRVNSPPGQYFSPDLDCMIMVAAQEGPTAFYKGFPSFLRGSNNVVMFVYEQLKRA 300
236 VKTRFINSPPGQYKSPVNCAMKVFTEGPTAFKGLVPSFLRGSNNVIMFVCFEQLKRB 295

QY 301 LMK 303
DB 296 LSK 298

RESULT 3

A22446
uncoupling protein - rabbit

C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 25-Sep-1989 #sequence revision 25-Sep-1989 #text_change 18-Feb-2000
C.Accession: A22446
R.Balogh, A.G.; Ridley, R.G.; Patel, H.V.; Freeman, K.B.

Biochem. Biophys. Res. Commun. 161, 156-161, 1989

A.Title: Rabbit brown adipose tissue uncoupling protein mRNA: use of only one of two po
A.Reference number: A22446; MUID:89273628; PMID:2730654

A.Accession: A22446
A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-306 <BAL>
A.Cross-references: GB:X14696

C.Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C.Keywords: duplication; mitochondrion; transmembrane protein
F.10-103/Domain: ADP,ATP carrier protein repeat homology <ACPI>
F.109-201/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F.208-295/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 55.9%; Score 905; DB 2; Length 306;
Best Local Similarity 57.8%; Pred. No. 1.6e-75;
Matches 175; Conservative 49; Mismatches 73; Indels 6; Gaps 3;

QY 1 MVLKSDVPPPTMAVVFLLAGTAAACFADLVTPPLDTAKVRLIOGQENQAVQARLVOYRG 60
1 MGLTASDVHPTLGLVQLFSAGIACADLVITPPLDTAKVRLVOQS--CPTSSVIRYKG 57
DB 1 VGTGTLTWRTEGPCSPYNGLVAGLQROWSPASIRIGLYDSVKQYTPKGDNSLITRI 120
61 VGTGTLTWRTEGPCSPYNGLVAGLQROWSPASIRIGLYDSVKQYTPKGDNSLITRI 120
DB 58 VLGTTTAAVKTBERMGLKSGLPAGLQROISASLRIGLVDTVQEFITAGETAPSLGSKI 116
121 LAGCTTGAAVTCAGPTDVVKVRFQASIHGSPRSRKYSGTMDAYRTTAREGVRLGK 180
117 LAGLTGGVAVFICGPTLVKVRLLQASHLGLKIP--RYGTGNAYRIIATTEGLTGLWK 174

DB 181 GTLPNIMRNATVNCAGVVTYDILKEKLDVHLLTNPFCHEFVSAGFCATVVASPVY 240
175 GTLPNIMRNATVNCAGVVTYDILKEKLPVKNLADVDVPCHLISALIAFCATVVASPVY 234
DB 241 VKTRVNSPPGQYFSPDLDCMIMVAAQEGPTAFYKGFPSFLRGSNNVVMFVYEQLKRA 300
235 VKTRFINSPPGQYKSPVNCAMKVFTEGPTAFKGLVPSFLRGSNNVIMFVCFEQLKRB 294
QY 301 LMK 303
DB 295 LMR 297

RESULT 4
A26294
uncoupling protein - rat

N.Alternate names: UCP
C.Species: Rattus norvegicus (Norway rat)
C.Date: 22-Jul-1987 #sequence revision 22-Jul-1987 #text_change 18-Feb-2000
C.Accession: A26294; A29278; S03842; A61566
R.Bouillaud, F.; Weisenbach, J.; Ricquier, D.

J. Biol. Chem. 261, 1487-1490, 1986

A.Reference number: A26294; MUID:86111804; PMID:3753702

A.Accession: A26294
A.Molecule type: mRNA

A.Residues: 1-307 <BOU>
A.Cross-references: GB:M1814; NID:g207556; PIDN:AAA19671.1; PID:g207557

R.Ridley, R.G.; Patel, H.V.; Geisler, G.B.; Morton, R.C.; Freeman, K.B.
Nucleic Acids Res. 14, 4025-4035, 1986

A>Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoch

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F:209-236/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 53.9%; Score 873.5; DB 2; Length 307;
Best Local Similarity 56.8%; Pred. No. 1.3e-72;
Matches 172; Conservative 45; Mismatches 81; Indels 5; Gaps 2;

QY 1 MVGLKPSVPPPMVKFLGAGTAACFADLVTPPTDPAKRLQIOGENAVQTAARLVQYRG 60
DB 1 MNPPTSTVHPTMGKIRISAGVACLAADITPPTDPAKRLQIOGENAVQTAARLVQYRG 57
QY 61 VLGTLLMTVTEGPCSPYNGVLVAGLQIQMSPASIRIGLYDSVKQYVTPKGDNSLTTRI 120
DB 58 VLGTLLMTVTEGPCSPYNGVLVAGLQIQMSPASIRIGLYDSVKQYVTPKGDNSLTTRI 117
QY 121 LAGCTGMAVTAQCPQVTVKVRPAPASIHLSGSRSDRYSGMDVRYTIAREGRGLMK 180
DB 118 SAGLMTGVAVFQGTPEVVKVRLQAQSHLGIRK-RTGTYNAYRLIATTESFTLMK 175
QY 181 GTLPIMENATVNCAEVVTYDLKEKLDYHLITDNPCHFEVSARFAGCATVVASPYDV 240
DB 176 GTTPPLANVILNCELVITYDLMKALVNNQILDADVCHLSAFAVAGCTTFLASPADV 235
QY 241 VKTIRYNSPPQGYFSPDLQMTKMAQEGPTAFYKGFPTSPFLRLGSMNVMPYTYEQIKRA 300
DB 236 VKTIRYNSPPQGYFSPDLQMTKMAQEGPTAFYKGFPTSPFLRLGSMNVMPYTYEQIKRA 295
QY 301 LMK 303
DB 236 LSK 298

RESULT 7

uncoupling protein - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Jun-2000
A:Accession: S03603; S05075
R:Castella, L.; Bouillaud, F.; Forest, C.; Ricquier, D.
Nucleic Acids Res. 17, 2131, 1989
A:Title: Nucleotide sequence of a cDNA encoding bovine brown fat uncoupling protein. Hom
A:Reference number: S03603; MUID:89183626; PMID:2928121
A:Accession: S03603
A:Molecule type: mRNA
A:Residues: 1-288 <CAS>
A:Cross-references: EMBL:X14064; NID:91495201; PIDN:CAA32227.1; PID:91495202
R:Ricquier, D.
submitted to the EMBL Data Library, January 1989
A:Reference number: S05075
A:Accession: S05075
A:Molecule type: mRNA
A:Residues: 1-195, 201, 'T', 203, 'RCC', 204-288 <RIC>
A:Cross-references: EMBL:X14064
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:1-87/Domain: ADP, ATP carrier protein repeat homology (fragment) <ACP1>
F:92-184/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F:191-277/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 52.2%; Score 846; DB 2; Length 288;
Best Local Similarity 58.9%; Pred. No. 4.1e-70;
Matches 168; Conservative 46; Mismatches 61; Indels 10; Gaps 5;

QY 20 AGTAACFADLVTPPTDPAKRLQIOGENAVQTAARLVQYRGVLTLLMTVTEGPCSPY 79
DB 4 AGTAACFADLVTPPTDPAKRLQIOGENAVQTAARLVQYRGVLTLLMTVTEGPCSPY 60
QY 80 GVAGLQIQMSPASIRIGLYDSVKQYVTPKGDNSLTTRIAGCTTGAAVTAQCPQTV 139
DB 61 GLPAGLQIQMSPASIRIGLYDSVKQYVTPKGDNSLTTRIAGCTTGAAVTAQCPQTV 118
QY 140 VYRFGASVHL-GPSSRSRSGTMDVRYTIAREGRGLMKVLTLLMTVTEGPCSPY 198
DB 140 VYRFGASVHL-GPSSRSRSGTMDVRYTIAREGRGLMKVLTLLMTVTEGPCSPY 198

DB 119 VKRLQAQSHLGK---PRYGTYNAYRLIATTEGLTGMLKGTSPNLTNVIINCELV 175
QY 199 TYDLKEKLDYHLITDNPCHFEVSARFAGCATVVASPYDVVKYRNSPPQGYFSPDL 258
DB 176 TYDLKEKLDYHLITDNPCHFEVSARFAGCATVVASPYDVVKYRNSPPQGYFSPDL 235

QY 259 CMIDVAGEGPTAFYKGFPTSPFLRLGSMNVMPYTYEQIKRALMK 303
DB 236 CAMMLTREGSARFAGCATVVASPYDVVKYRNSPPQGYFSPDL 279

RESULT 8

uncoupling protein (clone Stucp7), mitochondrial - potato
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
A:Accession: T07793
R:Latol, W.; Klein, M.; Riemer, J.W.; Mueller-Roeber, B.; Fleury, C.; Bouillaud, F.;
Nature 389, 135-136, 1997
A:Title: A plant cold-induced uncoupling protein.
A:Reference number: Z16136; MUID:97441051; PMID:9296489
A:Accession: T07793
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-306 <LAL>
A:Cross-references: EMBL:Y11220; NID:92398828; PIDN:CAA72107.1; PID:92398829
A:Experimental source: cv. Desiree
C:Genetics:
A:Genome: nuclear
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: mitochondrion

Query Match 42.4%; Score 687; DB 2; Length 306;
Best Local Similarity 47.7%; Pred. No. 1.9e-55;
Matches 146; Conservative 49; Mismatches 101; Indels 10; Gaps 5;

QY 7 SDVPTMAVKFLGAGTAACFADLVTPPTDPAKRLQIOGENAVQTAARLVQYRGVLTITL 66
DB 10 SDI--SFAGIFASAFACFAEACTLPDITAKVRLQIOKKAEBGDGLPKRIGLGTVG 67
QY 67 TMVTEGPCSPYNGVLVAGLQIQMSPASIRIGLYDSVKQYVTPKGDNSLTTRIAGCT 125
DB 68 TIAKEGASLIMKGIIVPELRQCCTGGIRKIMTEVKNLYGKHVGVPLSKTILALT 127
QY 126 TGAAVTAQCPQVTVKVRPAPASIHLSGSRSDRYSGMDVRYTIAREGRGLMKVLT 185
DB 128 TGAAGTITANFTDPAKRLQIOGENAVQTAARLVQYRGVLTITLMTVTEGPCSPY 186
QY 186 IMRNAIVNCAEVVTYDLKEKLDYHLITDNPCHFEVSARFAGCATVVASPYDVVKTRY 245
DB 187 IGRNATINAAHLSAYDQKAVLRIPGPTDPAKRLQIOGENAVQTAARLVQYRGVLT 246
QY 246 MNSPPQGYFSPDLQMTKMAQEGPTAFYKGFPTSPFLRLGSMNVMPYTYEQIKRALMK 305
DB 247 MGD--SAKNTLDCVKTLDKNDGFLAFYKGFIPNFGRLGSMNVMPYTYEQIKRALMK 303
QY 306 MLRSP 311
DB 304 ---ESP 306

RESULT 9

uncoupling protein (imported) - Arabidopsis thaliana
N:Alternate names: protein P24822.70
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Nov-2000
A:Accession: T47570; T52023
C:Keywords: H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Queirer, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23016
A:Accession: T47570
A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-306 <BLO>
 A:Cross-references: EMBL:AL132957
 A:Experimental source: cultivar Columbia; BAC clone F24B22
 R. Laloi, M.
 Submitted to the EMBL Data Library, August 1997
 A:Reference number: Z25905
 A:Accession: T52023
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-306 <LAL>
 A:Cross-references: EMBL:AJ001264; PIDN:CAA04638.1
 C:Genetics:
 A:Map position: 3
 A:Intons: 26/3; 98/3; 125/1; 169/3; 202/3; 237/3; 263/3; 292/3
 A:Note: F24B2.70
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 42.1%; Score 682; DB 2; Length 306;
 Best Local Similarity 48.3%; Pred. No. 5.5e-55;
 Matches 146; Conservative 46; Mismatches 100; Indels 10; Gaps 6;

QY 1 MVLGKPSD--VPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVQTARLVQY 58
 DB 1 MVAAGSDLSLPKTFAC-----SAFAACVGEVCTIPDITAKVRLQIQ-KSALAGDVTLPKY 55
 QY 59 RGVLTITLMTWTEGPCSPYNGVLVAGLQROMSPASIRIGLYDSVKOYTPKG-ADNSSLT 117
 DB 56 RGLGTGTIAREEGIRSLMKGVVPGILHROCLFGLGILGMVEPKNIYVKGDFVGDVPLS 115
 QY 118 TRIAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRKSGTMDAYRTIAREBGVRG 177
 DB 116 KTLIAGLTGALGIMVNPDLVVKVRLQABGKLA-AGAPRRISGALNASTIYRQEGVRA 174
 QY 178 LMKGTLPNIRNAIVNCAEVVYDILKEKLDYHLTDNPFCHVSAFGAGCATVVASP 237
 DB 175 LMTGLGNVARNAINAAELASDYQVETILKIPGFTDNVVTIISGLAGFPAVCIGSP 234
 QY 238 VDVVKTRRYNSPPGQYFSPDCKIKVNAOEGPFAFYKGFPSFLRLGSNNVVFVYEQ 297
 DB 235 VDVVKSRMMD--SGAYKGTIDCFVKTLKSDGPMAFYKGFIPNFGRLGSNNVIMFLTEQA 293
 QY 298 KR 299
 DB 294 KK 295

RESULT 10

T52024
 uncoupling protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
 C:Accession: T52024
 R:Maiz, I.G.; Benedetti, C.E.; Leite, A.; Turchinelli, S.R.; Vercesi, A.E.; Arruda, P.
 FEBS Lett. 429, 403-406, 1998
 A:Title: AtPUMP: an Arabidopsis gene encoding a plant uncoupling mitochondrial protein.
 A:Reference number: Z22968; MUID:9662458; PMID:9662458
 A:Accession: T52024
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-306 <MAI>
 A:Cross-references: EMBL:AJ23983; PIDN:CAA11757.1
 C:Genetics:
 A:Gene: PUMP
 C:Function:
 A:Description: may play a role in heat-requiring physiological events
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 41.5%; Score 673; DB 2; Length 306;
 Best Local Similarity 48.0%; Pred. No. 3.7e-54;
 Matches 145; Conservative 46; Mismatches 101; Indels 10; Gaps 6;

QY 1 MVLGKPSD--VPPTMAVKFLGAGTACFADLVTPPLDTAKVRLQIQENQAVQTARLVQY 58

DB 1 MVAAGSDLSLPKTFAC-----SAFAACVGEVCTIPDITAKVRLQIQ-KSALAGDVTLPKY 55
 QY 59 RGVLTITLMTWTEGPCSPYNGVLVAGLQROMSPASIRIGLYDSVKOYTPKG-ADNSSLT 117
 DB 56 RGLGTGTIAREEGIRSLMKGVVPGILHROCLFGLGILGMVEPKNIYVKGDFVGDVPLS 115
 QY 118 TRIAGCTTGAMAVTCAOPTDVVKVRFQASIHGSPSRDRKSGTMDAYRTIAREBGVRG 177
 DB 116 KTLIAGLTGALGIMVNPDLVVKVRLQABGKLA-AGAPRRISGALNASTIYRQEGVRA 174
 QY 178 LMKGTLPNIRNAIVNCAEVVYDILKEKLDYHLTDNPFCHVSAFGAGCATVVASP 237
 DB 175 LMTGLGNVARNAINAAELASDYQVETILKIPGFTDNVVTIISGLAGFPAVCIGSP 234
 QY 238 VDVVKTRRYNSPPGQYFSPDCKIKVNAOEGPFAFYKGFPSFLRLGSNNVVFVYEQ 297
 DB 235 VDVVKSRMMD--SGAYKGTIDCFVKTLKSDGPMAFYKGFIPNFGRLGSNNVIMFLTEQA 293
 QY 298 KR 299
 DB 294 KK 295

RESULT 11

JC7553
 brain mitochondrial carrier protein-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: JC7553
 R:Mizuno, T.; Miura-Suzuki, T.; Yamaehta, H.; Mori, N.
 Biochem. Biophys. Res. Commun. 278, 691-697, 2000
 A:Title: Distinct regulation of brain mitochondrial carrier protein-1 and uncoupling pr
 A:Reference number: JC7553; MUID: 20549014; PMID:11095970
 A:Accession: JC7553
 A:Molecule type: mRNA
 A:Residues: 1-325 <MIZ>
 A:Cross-references: GB:AF300424
 A:Experimental source: strain Male Wistar/SF
 C:Comment: This protein, a member of mitochondrial uncoupling protein family, has the rc
 ty to uncouple oxidative phosphorylation in yeast.
 C:Genetics:
 A:Gene: bmcpl
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: brain; carrier protein; mitochondrion

Query Match 32.3%; Score 524; DB 2; Length 325;
 Best Local Similarity 38.8%; Pred. No. 2.1e-40;
 Matches 112; Conservative 60; Mismatches 101; Indels 16; Gaps 5;

QY 17 FLGAGTACFADLVTPPLDTAKVRLQIQENQAVQTARLVQYRGVLTITLMTWTEGPCS 76
 DB 44 FVVGGLASIVAEFGTPEVDLTTRLOVQOSIDVR-FKEIKYGMFALPRIYREEGILA 102
 QY 77 PNGGLVAGLQROMSPASIRIGLYDSVKOYTPKGNADSSLTTRIILAGCTTGAMAVTCAOP 136
 DB 103 LYSIGLAPALRKQASYGITIKIGIQLKRLVER-LEDETILLINWICGVSVISSTIANP 161
 QY 137 TDVVKVRFQASIHGSPSRDRKSGTM-DAYRTIAREBGVRGLMKGTLPNIRNAIVNCA 195
 DB 162 TDVLKIRMQAGSL-----FGSWIGSFIDYQEGRTGLMRGVVPTAORAIIVGV 213
 QY 196 EVVTVYDILKEKLDYHLTDNPFCHVSAFGAGCATVVASPDVVKTRRYNSPP----- 250
 DB 214 ELVPYDITRKHLVSGMLGDTILTHFVSSFTGAGALASNPDVVKTRRYNSPP----- 273
 QY 251 GQYFSPDCKIKVNAOEGPFAFYKGFPSFLRLGSNNVVFVYEQ 299
 DB 274 DLKGTIDGLIKMKHGFALYKGFPMWRLKGPNNIIFFIYEQ 322

RESULT 12

T05577

uncoupling protein homolog F22K18.230 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 04-Mar-2000

C:Accession: T05577

R:Byan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hohnsbeil, J.; Mewes, H.W.; Mayer, K.F.

submitted to the Protein Sequence Database, February 1999

A:Reference number: 215419

A:Accession: T05577

A:Residues: 1-313 <BEV>

A:Cross-references: EMBL:AL035356

A:Experimental source: cultivar Columbia; BAC clone F22K18

C:Genetics:

A:Map position: 4

A:Note: F22K18.230

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 30.9%; Score 500.5; DB 2; Length 313;

Best Local Similarity 36.7%; Pred. No. 2.9e-38;

Matches 114; Conservative 51; Mismatches 123; Indels 23; Gaps 3;

13 MAVK-FLAGTACPADLVTPPLDTAKVRLQIQENQAVQTARL-----55

1 MGVSFVSGIASVIAAGSTHPLDLIKVRLQHGAPSTTTTLRPLALPNSSPAAL 60

56 -----VQYRGVLTITLWVTEGPCSPYNGVLVAGLQRMSPASIRIGLYDSVKQVYTPKG 110

61 ETTSTVPKVPISLGINIVKSGAALRSVGSATILRLQVLTSTMGLEYLVKNKWTPE 120

111 ADNSLITRIILAGCTTGAMAVTCAOPTDVVKVFPQASIHLPSSDRKSGTMDAYRTIA 170

121 SKGLMSRKIGAGLVAGGCAVGNPDAVAMRMQADGRL-PLAQRVYAGVGDALRSRV 179

171 REGRGRLMKGLPIMRAIYCAEVYTDILKELLDYHLITDNFPCHVSAFGACATVVASPDVVKTRYNN 230

180 KEEGVTSMRGSALTINRMIVTAQLASVYDFKKGITLNGVMNGLGTHVVASPAAGFV 239

231 ATTVASPDVVKTRYNNSPGQYFSPIDCMIKVAGQEGTAFYKGFSTFLTSGSNVVM 290

240 ASVASNPVDVITKTRVNMKVGAVDQAMPDAVKTVAEGMALYKGFVPTVCGQSPFTVL 299

291 FVTYEQLRKAL 301

300 FVTLEQVRKLL 310

Db

RESULT 13

H86274

FAL19.22 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001

C:Accession: H86274

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MID:21016719; PMID:11130712

A:Accession: H86274

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-305 <STO>

A:Cross-references: GB:AE005172; NID:g5080790; PIDN:AAD39300.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 29.5%; Score 478.5; DB 2; Length 305;

Best Local Similarity 37.0%; Pred. No. 2.9e-36;

Matches 108; Conservative 49; Mismatches 126; Indels 9; Gaps 4;

11 PTMAVKFAGTACPADLVTPPLDTAKVRLQIQENQAVQTARLVQYRGVLTITLWVR 70

11 PT-GRILLASLMSVASTFTPLDKTKMQLGSGSASAHN1-----GAFVSESLAR 65

71 TEGPCSPYNGVLVAGLQRMSPASIRIGLYDSVKQVYTPKGADNS--LITRIILAGCTTG 127

66 KEVIGLYKGLSPALIRHLFTPIRIIGENLKLIVASETNBSLPLATKALVGFSG 125

128 AMAVTCAOPTDVVKVFPQASIHLPSSDRKSGTMDAYRTIAEEGRGLMKGLPIM 187

126 VIAQVVASPADLVKRMQADGRLVSQGLKPRYSGPIAEFTKILQSEGVGLMKGLVFNQ 185

188 RNATVNCAEVYTDILKELLDYHLITDNFPCHVSAFGACATVVASPDVVKTRYNN 247

186 RAFLVMGELACVHAHFVLDKIAEDNIRAHILASISGLASTSLSCPADVKTTRMNN 245

248 SPFGQ-YFSPIDCMIKVAGQEGTAFYKGFSTFLTSGSNVVMFVTEQLK 298

246 QENAVVNSYDCLVKTVEGIRALMWGFPTWARLQPMQFVFWVSYEKER 297

Db

RESULT 14

H84613

hypothetical protein At2g22500 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: H84613

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayan, L.; Tallon,

er, D.; Merlan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MID:20083487; PMID:10617137

A:Accession: H84613

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-313 <STO>

A:Cross-references: GB:AE002093; NID:g4544443; PIDN:AAD22351.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g22500

A:Map position: 2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 29.2%; Score 472.5; DB 2; Length 313;

Best Local Similarity 36.9%; Pred. No. 1.1e-35;

Matches 114; Conservative 49; Mismatches 121; Indels 25; Gaps 6;

13 MAVK-FLAGTACPADLVTPPLDTAKVRLQIQENQAVQT-----ARLVQYR-----59

1 MGLKFAAGAGIASVIAAGSTHPLDLIKVRLQHGAPSTTTTLRPLALPNSSPAAL 60

60 --GVLTITLWVTEGPCSPYNGVLVAGLQRMSPASIRIGLYDSVKQVYTPKGADNSLT 117

61 RVGVIGVSRILIREGMAALFSGVATVLRQLTVSTTNGLYDILKGETDDETKMPLM 120

118 TRIILAGCTTGAMAVTCAOPTDVVKVFPQASIHLPSSDRKSGTMDAYRTIAEEGRVAG 177

121 KTIIGAGIAGAGAAVGNPADAVMRMQADGRL-PLTDRNRYKSVLDATQMKIRGEVTS 179

178 LMKGLTPMIRNAIVNCAEVYTDILKELLDYHLITDNFPCHVSAFGACATVVASPD 237

180 LMRGSLITINRMALVTSSQLASVDSVETILEKGLIKDGLGTHVASFAAGFVASVASNP 239

238 VDVVKTRYNN-----SPGQYFSPIDCMIKVAGQEGTAFYKGFSTFLTSGSNVVM 290

240 VDVVKTRYNN-----SPGQYFSPIDCMIKVAGQEGTAFYKGFSTFLTSGSNVVM 290

291 FVTYEQLRKAL 299

298 FVTLEQVRKLL 306

Db

```

RESULT 15
T15253
hypothetical protein K07B1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C:Accession: T15253
R:Pauley, A.; Gattung, S.
Submitted to the EMBL data library, May 1997
A:Description: The sequence of C. elegans cosmid K07B1.
A:Reference number: Z18317
A:Accession: T15253
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-343 <PAU>
A:Cross-references: EMBL:AF003364; NID:G2088617; PID:G2088821; PIDD:AAB54239.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone K07B1
C:Genetics:
A:Gene: CESP:K07B1.3
A:Map position: 5
A:Introns: 81/1; 131/3; 236/3; 279/2
C:Superfamily: ADP_ATP carrier protein; ADP_ATP carrier protein repeat homology

Query Match      27.1%; Score 439; DB 2; Length 343;
Best Local Similarity 33.3%; Pred. No. 1.5e-32;
Matches 98; Conservative 56; Mismatches 118; Indels 22; Gaps 3;

    22 TAACFADIVTPPLDPAKVRLQIOGENOAQTARLVGYRGVLATLLTVNRTGPSPPYNGL 81
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |
    49 TRALVAELVTVPLDTITKTRLQIARNKKFTKGIMWQ-----VTYDIRREGAMALMTGV 102
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

    82 VAGLCROMSFPASIRGLGYDSVKQVTPRKGDNS-SLTRILAGCTGTMAATCAOPTDV 140
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |
    103 APATRNHTIYTGIRGAAYEQIRLLTFNKVEKSPFLMYSMLCGAPSGIIAQFAASPVDLV 162
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

    141 KYRFQASITHLPSSRSRDRCXSGTMADAVRTIAREEGVRGLMKSTPLPINMNATLVNCSEVVTY 200
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |
    163 KVQMOMBEGRRLQOKPLRYTGATTCDFRSLYTKGFGLMIGMIPRCQDAALLNNADIAITY 222
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

    201 DLAKKLIDLHYLLTDNPFCHPVSAFGAGFCATVVASPYDVVYKTRYM----- 246
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

    223 DSVKGLGLDNDELKONWTLTHAVASACGLAAIALVISLPBDVVKTRMMDOIRHEDLAKMHK 282
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

    247 -NSPPGQYFSPLDCMIKNVAOGRPAFYKGGTPPSLTLSGSNNVMVFUYVEDOLK 299
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

    283 KNTHADVLRKGVVDDCYIKLIINEGFPSLYKGLPSPSTRAPWSLTFWVSYEIEIRK 336
       ||| : | : | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: May 17, 2004, 11:53:55
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:49:15 ; Search time 45 Seconds
(without alignments)
2187.593 Million cell updates/sec

Title: US-09-423-410-4
Perfect score: 1620
Sequence: 1 MWGLKPSDVPPTMAVKFLGA.....TYEQKRAIMKYQMLRESPP 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_viruses:*
16: SP_bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|--------------------|
| 1 | 1370 | 84.6 | 312 | 11 | Q7TNY4 | Q7TNY4 dicostonyx |
| 2 | 1350 | 83.3 | 299 | 11 | Q9ER16 | Q9ER16 phodopus su |
| 3 | 1178 | 72.7 | 310 | 6 | Q7YRF3 | Q7YRF3 antechinus |
| 4 | 1173.5 | 72.0 | 307 | 13 | Q7ZXN1 | Q7ZXN1 xenopus lae |
| 5 | 1166.5 | 72.4 | 307 | 13 | Q90X50 | Q90X50 melagris g |
| 6 | 1163.5 | 71.8 | 309 | 11 | Q9R246 | Q9R246 mus musculu |
| 7 | 1162.5 | 71.8 | 307 | 13 | Q9DDT7 | Q9DDT7 gallus gall |
| 8 | 1159.5 | 71.6 | 307 | 13 | Q8ATM4 | Q8ATM4 gallus gall |
| 9 | 1158.5 | 71.5 | 309 | 11 | Q8CBU0 | Q8CBU0 mus musculu |
| 10 | 1158.5 | 71.5 | 309 | 11 | Q9ER17 | Q9ER17 phodopus su |
| 11 | 1141 | 70.4 | 304 | 13 | Q9ER90 | Q9ER90 eupetomena |
| 12 | 1127.5 | 69.6 | 309 | 13 | Q7ZVP4 | Q7ZVP4 brachydanto |
| 13 | 1026 | 63.3 | 274 | 6 | Q7YRF2 | Q7YRF2 emithopeis |
| 14 | 1004.5 | 62.0 | 273 | 6 | Q9XSE1 | Q9XSE1 bos taurus |
| 15 | 929 | 57.3 | 193 | 6 | Q9NID8 | Q9NID8 macaca mula |
| 16 | 925.5 | 57.1 | 309 | 6 | Q9GMZ1 | Q9GMZ1 canis famli |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 879.5 | 54.3 | 307 | 11 | Q9ER18 | Q9ER18 phodopus su |
| 18 | 866.5 | 53.5 | 307 | 11 | Q8K404 | Q8K404 dicostonyx |
| 19 | 834.5 | 51.5 | 224 | 13 | Q8QG96 | Q8QG96 pagrus majo |
| 20 | 781.5 | 48.2 | 209 | 13 | Q7TIC5 | Q7TIC5 brachydanto |
| 21 | 713.5 | 44.0 | 304 | 10 | Q8LNZ1 | Q8LNZ1 heliodicer |
| 22 | 687 | 42.4 | 306 | 10 | Q24391 | Q24391 solanum tub |
| 23 | 687 | 42.4 | 306 | 10 | Q8SA58 | Q8SA58 lycopersico |
| 24 | 684.5 | 42.3 | 300 | 10 | Q9AVG1 | Q9AVG1 oryza sativ |
| 25 | 682 | 42.1 | 306 | 10 | Q81845 | Q81845 arabidopsis |
| 26 | 681.5 | 42.1 | 310 | 10 | Q8S4C4 | Q8S4C4 zea mays (m |
| 27 | 675.5 | 41.7 | 303 | 10 | Q9MBE7 | Q9MBE7 sympllocarpu |
| 28 | 673 | 41.5 | 306 | 10 | Q65623 | Q65623 arabidopsis |
| 29 | 639 | 39.4 | 305 | 10 | Q9ZWG1 | Q9ZWG1 arabidopsis |
| 30 | 619.5 | 38.2 | 293 | 10 | Q9AVG2 | Q9AVG2 oryza sativ |
| 31 | 615 | 38.0 | 286 | 10 | Q9FX05 | Q9FX05 triticum ae |
| 32 | 606 | 37.4 | 286 | 10 | Q9FX06 | Q9FX06 triticum ae |
| 33 | 592 | 36.5 | 268 | 10 | Q9MBE6 | Q9MBE6 sympllocarpu |
| 34 | 545 | 33.6 | 154 | 6 | Q9NID9 | Q9NID9 macaca mula |
| 35 | 541 | 33.4 | 242 | 10 | Q94F06 | Q94F06 mangifera i |
| 36 | 538 | 33.2 | 241 | 10 | Q8W1A4 | Q8W1A4 glycine max |
| 37 | 537 | 33.1 | 241 | 10 | Q8W1A3 | Q8W1A3 glycine max |
| 38 | 524 | 32.3 | 322 | 11 | Q9JMH0 | Q9JMH0 rattus norv |
| 39 | 524 | 32.3 | 325 | 11 | Q9EP88 | Q9EP88 rattus norv |
| 40 | 521 | 32.2 | 353 | 11 | Q8CJ24 | Q8CJ24 mus musculu |
| 41 | 521 | 32.2 | 356 | 11 | Q8CJ23 | Q8CJ23 mus musculu |
| 42 | 515 | 31.8 | 155 | 6 | Q9N1E0 | Q9N1E0 macaca mula |
| 43 | 514.5 | 31.8 | 291 | 6 | Q8HXE3 | Q8HXE3 macaca fasc |
| 44 | 510.5 | 31.5 | 291 | 11 | Q9CR58 | Q9CR58 mus musculu |
| 45 | 501 | 30.9 | 337 | 10 | Q9PYE8 | Q9PYE8 arabidopsis |

ALIGNMENTS

| RESULT 1 | Q7TNY4 | PRELIMINARY; | PRT; | 312 AA. |
|----------|---|--------------|------|---------|
| ID | Q7TNY4 | | | |
| AC | Q7TNY4 | | | |
| DT | 01-OCT-2003 (T-EMBLrel. 25, Created) | | | |
| DT | 01-OCT-2003 (T-EMBLrel. 25, Last sequence update) | | | |
| DT | 01-OCT-2003 (T-EMBLrel. 25, Last annotation update) | | | |
| DE | Uncoupling protein 3. | | | |
| DE | Dicostonyx greenlandicus (northern collared lemming). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae; | | | |
| OC | Dicostonyx. | | | |
| RN | NCBI_TaxID=89553; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Blaylock M.L., Wang R., Nagy T.R.; | | | |
| RT | "Expression of Ucp3 mRNA during weight gain and loss, cold exposure | | | |
| RT | and fasting in the collared lemming." | | | |
| RL | Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AY326457; AAB94991.1; - | | | |
| SQ | SEQUENCE 312 AA; 34442 MW; 6EBAF7F4E4B62DE5 CRC64; | | | |

| | | | | |
|-----------------------|------------------|--|-----------|-------------|
| Query Match | 84.6%; | Score 1370; | DB 11; | Length 312; |
| Best Local Similarity | 84.8%; | Pred. No. 3.1e-120; | | |
| Matches 266; | Conservative 17; | Mismatches 23; | Indels 8; | Gaps 3; |
| QY | 1 | MWGLKPSDVPPTMAVKFLGAGTACFADLVTPPELDTAKYRLQIQENQAVQTARLVQYRG 60 | | |
| DB | 1 | MWGLQPSSEVPPTVVFVFLGATGACFADLLTFPLDTAKYRLQIQENQAVQYRG 57 | | |
| QY | 61 | VLGTTITLMTREPCSPNGVAGLOROMSPASIRIGLVDSVQVYTPPGADNSSLTRT 120 | | |
| DB | 58 | VLGTTITLMTREPCSPNGVAGLOROMSPASIRIGLVDSVQVYTPPGADNSSLTRT 117 | | |
| QY | 121 | LACCTGAMAVTGAOPTDVVKYRFQASIRHLGSPRSRDKTSGTWDAYRTTAREGVLWK 180 | | |
| DB | 118 | LACCTGAMAVTGAOPTDVVKYRFQAMIRLG-TGSRKTRGTADAYRTTAREGVLWK 176 | | |
| QY | 181 | GLPLNTRNAIVNCAEVVTYDILKEKLLDYHLTLTNDPCHFEVSAFGACATVVASPVV 240 | | |

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Db      177 GTWPITNATNATNCAMWVYDILKEKLDLSHLFTNPFCHFYSAAGAFCAIVVSPDV 236
Qy      241 VKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQLKRA 300
Db      237 VKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQLKRA 296
Qy      301 ----LMKVOMLRESPE 312
Db      297 LSKLMKVOMLRESPE 312

RESULT 2
Q9ER16 PRELIMINARY; PRT; 299 AA.
ID Q9ER16;
AC Q9ER16;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Uncoupling protein 3 (Fragment).
OS Phodopus sungorus (Striped hairy-footed hamster) (Djunganian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Phodopus.
OC NCBI_TaxID=10044;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Brown adipose tissue;
RA von Prun C., Burkert M., Gessner M., Klingenspor M.;
RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling
   proteins in the Djunganian hamster.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF272426; AAG33985.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0006839; P:mitochondrial transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mtc_carrier.
DR InterPro: IPR002030; Mtc_uncoupling.
DR Pfam: PF00153; mltc_carrier_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Membrane; Transmembrane; Transport.
DR FT NON_TER 299
SQ SEQUENCE 299 AA; 32784 MW; ABS0947B4DDC49A0 CRC64;

Query Match      83.3%; Score 1350; DB 11; Length 299;
Best Local Similarity 86.0%; Pred. No. 2.2e-118;
Matches 259; Conservative 16; Mismatches 22; Indels 4; Gaps 2;

Qy      1  MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLIOGSENAVQTARLVQYRG 60
      1  MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLIOGSENAVQTARLVQYRG 57
Db      61 VLGITLTWRTGPGSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLTTRI 120
      58 VLGITLTWRTGPGSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLTTRI 117
Qy      121 LAGCTTGAAVCAOQPTDVVKVRFQASIHLSRSRSGTMDAVRTIAREEGVGLK 180
      121 LAGCTTGAAVCAOQPTDVVKVRFQASIHLSRSRSGTMDAVRTIAREEGVGLK 176
Db      118 LAGCTTGAAVCAOQPTDVVKVRFQASIHLSRSRSGTMDAVRTIAREEGVGLK 176
      181 GTLPNIRNAIVNCAEVVYDILKEKLDLSHLFTNPFCHFYSAAGAFCAIVVSPDV 240
      177 GTMPNITRAIVNCAEVVYDILKEKLDLSHLFTNPFCHFYSAAGAFCAIVVSPDV 236
Qy      241 VKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQLKRA 300
      241 VKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQLKRA 300

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Db      237 VKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQLKRA 296
Qy      301 L 301
Db      297 L 297

RESULT 3
QYRF3 PRELIMINARY; PRT; 310 AA.
ID QYRF3;
AC QYRF3;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Uncoupling protein 2.
OS Antechinus flavipes (Yellow-footed marsupial mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
OC NCBI_TaxID=38775;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RA Jastrict M., Withers K., Klingenspor M.;
RT "Identification of UCP2 in the marsupial Antechinus flavipes.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY233003; AAP44414.1; -.
SQ SEQUENCE 310 AA; 33304 MW; 11917916F30E54F CRC64;

Query Match      72.7%; Score 1178; DB 6; Length 310;
Best Local Similarity 72.6%; Pred. No. 3.4e-102;
Matches 228; Conservative 34; Mismatches 46; Indels 6; Gaps 3;

Qy      1  MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLIOGSENAVQTARLVQY 58
      1  MWGLKPSDVPPTMAVFLGAGTAACFADLVTFPLDTAKVRLIOGSENAVQTARLVQY 60
Db      59 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 118
      61 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 119
Qy      119 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 118
      119 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 118
Db      119 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 118
      120 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 116
Qy      120 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 118
      120 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 116
Db      120 RGVLTGTLTWRTEGPCSPYNGLVAGLQRONSFASIRIGLYDSYKQVYTPPGADNSLT 118
      179 WKGLPNIIRNAIVNCAEVVYDILKEKLDLSHLFTNPFCHFYSAAGAFCAIVVSPV 238
      177 WKGLPNIIRNAIVNCAEVVYDILKEKLDLSHLFTNPFCHFYSAAGAFCAIVVSPV 236
Qy      239 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 298
      239 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 296
Db      237 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 298
      237 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 296
Qy      239 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 298
      239 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 296
Db      237 DVKTRVNSPPGOYFSLPDCMIMKVAOEGPTAFYKGFSTPSFLRGSNNVVFYTYEQ 298
      297 RALMVKVOMLRESPE 312
      297 RALMVKVOMLRESPE 310

RESULT 4
Q7ZXN1 PRELIMINARY; PRT; 307 AA.
ID Q7ZXN1;
AC Q7ZXN1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Bmdryo;

```


RL FEBS Lett. 0:0-0(2002).
 DR EMBL; AB088685; BAC15532.1; --
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006413; P:translational initiation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR00794; Ketoacyl_synth.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001950; TIF_SUI1.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUCCOUPLING.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS01118; SUI1; 1.
 DR SEQUENCE 307 AA; 3316 MW; 33AC1CD66FC1A888 CRC64;

Query Match 71.6%; Score 1159.5; DB 13; Length 307;
 Best Local Similarity 71.5%; Pred. No. 1.8e-100;
 Matches 223; Conservative 39; Mismatches 43; Indels 7; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQEGNQAVOTARLVQYRG 60
 DB 1 MWGLKPEPEVPTAAVFPFAGTAACIADLITFPLDTAKVRLQIQEGVLRPSRTVTEVING 60
 QY 61 VGLTILTMVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSLTTR 120
 DB 61 VGLTILTMVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSLTTR 120
 QY 121 IAGCTTGAMAVTCAOPTDVVKVRFQASIHLP-SRSDRKYSGTMDAYRTIAREEGVGLM 179
 DB 121 IAGCTTGAMAVTCAOPTDVVKVRFQASIHLP-SRSDRKYSGTMDAYRTIAREEGVGLM 179
 QY 121 IAGCTTGAMAVTCAOPTDVVKVRFQASIHLP-SRSDRKYSGTMDAYRTIAREEGVGLM 179
 DB 121 IAGCTTGAMAVTCAOPTDVVKVRFQASIHLP-SRSDRKYSGTMDAYRTIAREEGVGLM 179
 QY 180 KGTLEINEMALVNCAEVTVYDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPD 239
 DB 180 KGTLEINEMALVNCAEVTVYDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPD 239
 QY 178 KGTLEINEMALVNCAEVTVYDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPD 237
 DB 178 KGTLEINEMALVNCAEVTVYDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPD 237
 QY 240 VKTRRYMNSPFGQYSPFLDCMIKMAVQEGPTAFYKGFPTSPFLRSGMNVVFTYEQLR 299
 DB 240 VKTRRYMNSPFGQYSPFLDCMIKMAVQEGPTAFYKGFPTSPFLRSGMNVVFTYEQLR 299
 QY 238 VKTRRYMNSPFGQYSPFLDCMIKMAVQEGPTAFYKGFPTSPFLRSGMNVVFTYEQLR 297
 DB 238 VKTRRYMNSPFGQYSPFLDCMIKMAVQEGPTAFYKGFPTSPFLRSGMNVVFTYEQLR 297
 QY 300 ALMKVQMLRESP 311
 DB 298 VVM---LARSAP 306
 RESULT 9
 Q8CBU0 PRELIMINARY; PRT; 309 AA.
 AC Q8CBU0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Uncoupling protein 2.
 GN UCP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RA MEDLINE=22354683; PubMed=1246651;
 RX THE PANOM Consortium,
 RA THE RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK035298; BAC29021.1; --
 DR MGD; MGI:109354; Ucp2.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUCCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR SEQUENCE 309 AA; 3338 MW; 6E6454DAC14D99DE CRC64;

Query Match 71.6%; Score 1159.5; DB 11; Length 309;
 Best Local Similarity 72.5%; Pred. No. 1.8e-100;
 Matches 227; Conservative 31; Mismatches 50; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQEGNQAVOTARLVQYRG 59
 DB 1 MWGLKPEPEVPTAAVFPFAGTAACIADLITFPLDTAKVRLQIQEGVLRPSRTVTEVING 60
 QY 60 GVLGTLTMVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSLTTR 119
 DB 61 GVLGTLTMVTEGPGSPYNGLVAGLQROMSFASIRIGLYDSVKQVYTPKADNSLTTR 119
 QY 120 ILAGCTTGAMAVTCAOPTDVVKVRFQASIHLP-SRSDRKYSGTMDAYRTIAREEGVGLM 179
 DB 120 ILAGCTTGAMAVTCAOPTDVVKVRFQASIHLP-SRSDRKYSGTMDAYRTIAREEGVGLM 179
 QY 180 KGTLEINEMALVNCAEVTVYDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPD 239
 DB 177 KGTSPNARMALVNCAEVTVYDILKEKLDYHLTDNPFCHVSAFGAGFCATVVASPD 236
 QY 240 VKTRRYMNSPFGQYSPFLDCMIKMAVQEGPTAFYKGFPTSPFLRSGMNVVFTYEQLR 299
 DB 237 VKTRRYMNSALQVYSAAGCALTMLRKEGPRAFYKGFPMPSFLRSGMNVVFTYEQLR 296
 QY 300 ALMKVQMLRESP 312
 DB 297 ALMAAYQSRAP 309
 RESULT 10
 Q9ER17 PRELIMINARY; PRT; 309 AA.
 AC Q9ER17;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Uncoupling protein 2.
 OS Phodopus sungorus (Striped hairy-footed hamster) (Djunganian hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Phodopus.
 NCBI_TaxID=10044;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA von Praun C.; Burkert M.; Gessner M.; Klingenspor M.;
 RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling
 RT proteins in the Djunganian hamster."
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 CC -1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF271264; AAC33984.1; --
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carri_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 SQ SEQUENCE 309 AA; 33359 MW; 9D9C4C1B169F2771 CRC64;

Query Match 71.5%; Score 1158.5; DB 11; Length 309;
 Best Local Similarity 72.2%; Pred. No. 2.3e-100;
 Matches 226; Conservative 33; Mismatches 49; Indels 5; Gaps 3;

QY 1 MVLKPSDVPPMTAKVFIAGTAACFADLVTFPPDTAKVRLQIQENQAVQTARLVQYR 59
 Db 1 MGLFAIDVPPATYKFLIAGTAACIADLITPPDTAKVRLQIQESQGLARTANAYRG 60
 QY 60 GVLGTLITWRTGEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPKGDNSLITRI 119
 Db 61 GVLGTLITWRTGEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPKGDNSLITRI 119
 QY 120 ILAGCTTGAMATCAOPTDVVVRFOASIHLPSSDRYSGTMDAYRTIAREEGVRLMK 179
 Db 120 ILAGCTTGAMATCAOPTDVVVRFOASIHLPSSDRYSGTMDAYRTIAREEGVRLMK 176
 QY 180 KGTLEINMNAIVNCAEVVYDILKEKLDYHLITDNPFCHVSAFGAGFCATVVASPYD 239
 Db 177 KGTLEINMNAIVNCAEVVYDILKEKLDYHLITDNPFCHVSAFGAGFCATVVASPYD 236
 QY 240 VKTRVYNSPPQGYSPFLDCMIRKVAQEGPTAFYKGFPTSPFLRSGMNVMTVYEQLR 299
 Db 237 VKTRVYNSALQGHYSAGHCALTMLRKSGPRAFYKGFPTSPFLRSGMNVMTVYEQLR 296
 QY 300 ALMKVQMLRESPP 312
 Db 297 ALMAAYESREAPF 309

RESULT 11

ID Q98T90 PRELIMINARY; PRT; 304 AA.
 AC Q98T90;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mitochondrial uncoupling protein UCP.
 OS Eupetomena macroura (swallow-tailed hummingbird).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Trochiliformes; Trochilidae;
 OC Eupetomena.
 OC NCBI_TaxID=153633;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vianna C.R., Hagen T., Zhang C.-Y., Bachman E., Boes O., Gereben B.,
 RA Morisco A.S., Lowell B.B., Biscudo J.B.P.W., Bianco A.C.;
 RT "Cloning and functional characterization of an uncoupling protein
 homolog in hummingbirds.";
 RL Physiol. Genomics (Online) 0:0-0(2001).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF255729; AAK1829.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006839; P:fatty acid biosynthesis; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006413; P:translational initiation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR00794; Ketoacyl_synth.
 DR InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001950; TIF_SUI1.
 DR Pfam; PF00153; mito_carri_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00606; B_KENOACYL_SYNTHASE; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS01118; SUI1_1; 1.
 DR Membrane; Transmembrane; Transport.
 SQ SEQUENCE 304 AA; 32833 MW; 3016453B21486795 CRC64;

Query Match 70.4%; Score 1141; DB 13; Length 304;
 Best Local Similarity 71.7%; Pred. No. 9.8e-99;
 Matches 215; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

QY 1 MVLKPSDVPPMTAKVFIAGTAACFADLVTFPPDTAKVRLQIQENQAVQTARLVQYR 60
 Db 1 MVALKSQMPPTAKIKPFSATACFADLVTFPPDTAKVRLQIQEVAIPVSGAVEYRG 60
 QY 61 VLGTLITWRTGEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPKGDNSLITRI 120
 Db 61 VLGTLITWRTGEGPCSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPKGDNSLITRI 120
 QY 121 ILAGCTTGAMATCAOPTDVVVRFOASIHLPSSDRYSGTMDAYRTIAREEGVRLMK 180
 Db 121 ILAGCTTGAMATCAOPTDVVVRFOASIHLPSSDRYSGTMDAYRTIAREEGVRLMK 178
 QY 181 GTPLEINMNAIVNCAEVVYDILKEKLDYHLITDNPFCHVSAFGAGFCATVVASPYD 240
 Db 179 GTPLEINMNAIVNCAEVVYDILKEKLDYHLITDNPFCHVSAFGAGFCATVVASPYD 238
 QY 241 VKTRVYNSPPQGYSPFLDCMIRKVAQEGPTAFYKGFPTSPFLRSGMNVMTVYEQLR 300
 Db 239 VKTRVYNSPPQGYSPFLDCMIRKVAQEGPTAFYKGFPTSPFLRSGMNVMTVYEQLR 298

RESULT 12

ID Q7ZVP4 PRELIMINARY; PRT; 309 AA.
 AC Q7ZVP4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC045464; AAH45464.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carri_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Hypothetical protein.
 SQ SEQUENCE 309 AA; 33766 MW; C10F7B4C1FECB829 CRC64;
 Query Match 69.6%; Score 1127.5; DB 13; Length 309;
 Best Local Similarity 72.2%; Pred. No. 1.9e-97;
 Matches 218; Conservative 33; Mismatches 48; Indels 3; Gaps 2;

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Db      1 MWGLKRPDVPPLTVKVLVSAGTAACTADIVTFPLDPAKRLIOIGEKAVTGAAGKGRYKG 60
OY      61 VGLTILMTWRTGSPGSPVNGVAGLQROMSPASIRIGLVDSYKQVYTPPGADNSLTTIRI 120
Db      61 VGLTILMTWRTGSPGSPVNGVAGLQROMSPASIRIGLVDSYKQVYTPPGADNSLTTIRI 119
OY      121 IAGCTTGAMAVTCAOPTDVVKYRFOASIRHGPSRSDRKYSCTMDAYRTIAREGVGWLWK 180
Db      120 IAGCTTGAMAVTCAOPTDVVKYRFOASIRHGPSRSDRKYSCTMDAYRTIAREGVGWLWK 177
OY      181 GTLPINMENAIVNCAEVVYDILKEKLLDYHLITDPCHFPVSAGFAGFCATYVASPVUV 240
Db      178 GTLPINMENAIVNCAEVVYDILKEKLLDYHLITDPCHFPVSAGFAGFCATYVASPVUV 237
OY      241 VTRTVNNSPPGOYFSPDLCKMKVNAQESPTAFYKGPSPSLRIGSNVVMFVYEQLKRA 300
Db      238 VTRTVNNSPPGOYFSPDLCKMKVNAQESPTAFYKGPSPSLRIGSNVVMFVYEQLKRA 297
OY      301 LM 302
Db      298 MM 299

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RESULT 13

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OYRPF2 07YRPF2 PRELIMINARY; PRT; 274 AA.
AC 07YRPF2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Uncoupling protein 2 (Fragment).
GN UCP2.
OS Smithopsis macroura (Stripe-faced dunbart).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorpha; Dasyuridae; Smithopsis.
OX NCBI_TaxID=9302;
RN 11
RP SOURCE FROM N.A.
RC TISSUE=Splice;
RA Jastrow M., Withers K., Klingenspor M.;
RT "Identification of UCP2 in Smithopsis macroura."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232996; AAP45779.1; -.
FT NON_TER 1
SQ SEQUENCE 274 AA; 29754 MW; 810DABA382B4A569 CRC64;

```

Query Match 63.3%; Score 1026; DB 6; Length 274;
 Best Local Similarity 72.2%; Pred. No. 5.4e-88;
 Matches 200; Conservative 32; Mismatches 41; Indels 4; Gaps 3;

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OY      37 AKRRLIOIGENQ-AVOTARLVQYRGVLTILMTWRTGSPGSPVNGVAGLQROMSPASIR 95
Db      1 AKRRLIOIGENQ-AVOTARLVQYRGVLTILMTWRTGSPGSPVNGVAGLQROMSPASIR 60
OY      96 IGLYDSVKQVYTPPKGADNSLTTIRILAGCTTGAMAVTCAOPTDVVKYRFOASIRHGPSRS 155
Db      61 IGLYDSVKQVYTPPKGADNSLTTIRILAGCTTGAMAVTCAOPTDVVKYRFOASIRHGPSRS 117
OY      156 DRKYSCTMDAYRTIAREBVGRLMKGTLPINMENAIVNCAEVVYDILKEKLLDYHLITD 215
Db      118 SRRYQGTMDAYRTIAREBVGRLMKGTLPINMENAIVNCAEVVYDILKEKLLDYHLITD 177
OY      216 NPECHVSAFAGFCATVVASPVVDVVKTRVNSPPGOYFSPDLCKMKVNAQESPTAFYKG 275
Db      178 DLPCHFTSAFAGFCATVVASPVVDVVKTRVNSATGQYASAGHCALTMKKEGPOAFYKG 237
OY      276 FTSPSLRIGSNVVMFVYEQLKRALMKVOMLRSEPF 312
Db      238 FMPSFLRIGSNVVMFVYEQLKRALMAARSRSEVP 274

```

RESULT 14

```

OYXSEI ID OYXSEI PRELIMINARY; PRT; 273 AA.
AC OYXSEI;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Uncoupling protein 2 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SOURCE FROM N.A.
RA Stone R.T., Rexroad C.E., Smith T.P.L.;
RT "Bovine UCP2 and UCP3 map to BTA15."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127029; AAD29672.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006839; P:mitochondrial transport; IEA.
DR GO; GO:006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002030; Mito_carrier.
DR Pfam; PF00153; mito_carrier.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS000215; MITOCH_CARRIER; 2.
FT NON_TER 1
SQ SEQUENCE 273 AA; 29638 MW; 40DAF6CB47AAB48 CRC64;

```

Query Match 62.0%; Score 1004.5; DB 6; Length 273;
 Best Local Similarity 71.5%; Pred. No. 5.6e-86;
 Matches 198; Conservative 29; Mismatches 45; Indels 5; Gaps 3;

```

OY      37 AKRRLIOIGENQ-AVOTARLVQYRGVLTILMTWRTGSPGSPVNGVAGLQROMSPASIR 95
Db      1 AKRRLIOIGENQ-AVOTARLVQYRGVLTILMTWRTGSPGSPVNGVAGLQROMSPASIR 60
OY      96 IGLYDSVKQVYTPPKGADNSLTTIRILAGCTTGAMAVTCAOPTDVVKYRFOASIRHGPSRS 155
Db      61 IGLYDSVKQVYTPPKGADNSLTTIRILAGCTTGAMAVTCAOPTDVVKYRFOASIRHGPSRS 116
OY      156 DRKYSCTMDAYRTIAREBVGRLMKGTLPINMENAIVNCAEVVYDILKEKLLDYHLITD 215
Db      117 GRRYQGTMDAYRTIAREBVGRLMKGTLPINMENAIVNCAEVVYDILKEKLLDYHLITD 176
OY      216 NPECHVSAFAGFCATVVASPVVDVVKTRVNSPPGOYFSPDLCKMKVNAQESPTAFYKG 275
Db      177 DLPCHFTSAFAGFCATVVASPVVDVVKTRVNSALQYSSAGHCALTMKKEGPOAFYKG 236
OY      276 FTSPSLRIGSNVVMFVYEQLKRALMKVOMLRSEPF 312
Db      237 FMPSFLRIGSNVVMFVYEQLKRALMAARSRSEVP 273

```

RESULT 15

```

OYXSEI ID OYXSEI PRELIMINARY; PRT; 193 AA.
AC OYXSEI;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Uncoupling protein 3 (Fragment).
GN UCP3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN 11
RP SOURCE FROM N.A.

```

RA Thompson G.M., Kelly L.J., Candelore M.R.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -! SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF202131; AAF34907.1; -.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.
 DR GO: GO:0005739; C: mitochondrial inner membrane; IEA.
 DR GO: GO:0005488; F: binding; IEA.
 DR GO: GO:0006839; P: mitochondrial transport; IEA.
 DR GO: GO:0006810; P: transport; IEA.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carr; 2.
 DR PRINTS: PR00784; MTNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transmembrane; Transport.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 193 AA; 20730 MW; 5D840DB668091DD CRC64;

Query Match 57.3%; Score 929; DB 6; Length 193;
 Best Local Similarity 95.3%; Pred. No. 4,4e-79;
 Matches 183; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```
QY 15 VKFLGAGTAACPADLVTPPLDPAKVRLOIQENQAVOTARLVQYRGVLTGTLTMVRTGEP 74
   |||||
DB 2 VKFLGAGTAACPADLVTPPLDPAKVRLOIQENQAVOTARLVQYRGVLTGTLTMVRTGEL 61
   |||||

QY 75 CSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPKGADNSSLTRILAGCTTGAMAVTCA 134
   |||||
DB 62 CSPYNGLVAGLQROMSPASIRIGLYDSVKQVYTPKGADNSSLTRILAGCTTGAMAVTCA 121
   |||||

QY 135 OPTDVVKTRFQASIHGSPSRDPRKYSGMTDAVRTIAREBGVRLKMTLPNIMRNAIVNC 194
   |||||
DB 122 OPTDVVKTRFQASIHGSSGSDRKYSGMTDAYRTIAREBGVRLKMTLPNIMRNAIVNC 181
   |||||

QY 195 AEVVTYDILKEK 206
   |||||
DB 182 AEVVTYDILKEK 193
   |||||
```

Search completed: May 17, 2004, 11:52:53
 Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OK protein - protein search, using sw model

Run on: May 17, 2004, 11:49:15 ; Search time 17 Seconds
(without alignments)
955.640 Million cell updates/sec

Title: US-09-423-410-4

Perfect score: 1620
Sequence: 1 MVGLKPSDVPPTMAVFLGA.....TYEQLKALMKQMLRESPP 312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1620 | 100.0 | 312 | 1 | UCP3_HUMAN |
| 2 | 1492.5 | 92.1 | 311 | 1 | UCP3_CANFA |
| 3 | 1457 | 89.9 | 306 | 1 | UCP3_PIG |
| 4 | 1419.5 | 87.6 | 311 | 1 | UCP3_BOVIN |
| 5 | 1386 | 85.6 | 308 | 1 | UCP3_RAT |
| 6 | 1373 | 84.8 | 308 | 1 | UCP3_MOUSE |
| 7 | 1165.5 | 71.9 | 309 | 1 | UCP2_MOUSE |
| 8 | 1160.5 | 71.6 | 309 | 1 | UCP2_PIG |
| 9 | 1156.5 | 71.4 | 309 | 1 | UCP2_RAT |
| 10 | 1149.5 | 71.0 | 309 | 1 | UCP2_HUMAN |
| 11 | 1145.5 | 70.7 | 309 | 1 | UCP2_CANFA |
| 12 | 1121 | 69.2 | 310 | 1 | UCP2_CYPCA |
| 13 | 1117 | 69.0 | 310 | 1 | UCP2_BRARB |
| 14 | 919 | 56.7 | 306 | 1 | UCP1_RABIT |
| 15 | 902.5 | 55.7 | 307 | 1 | UCP1_HUMAN |
| 16 | 898.5 | 55.5 | 306 | 1 | UCP1_RAT |
| 17 | 885.5 | 54.7 | 306 | 1 | UCP1_MOUSE |
| 18 | 869.5 | 53.7 | 306 | 1 | UCP1_MBSAU |
| 19 | 846 | 52.2 | 288 | 1 | UCP1_BOVIN |
| 20 | 521 | 32.2 | 325 | 1 | UCP5_MOUSE |
| 21 | 512 | 31.6 | 325 | 1 | UCP5_HUMAN |
| 22 | 475.5 | 29.4 | 323 | 1 | UCP4_HUMAN |
| 23 | 444 | 27.4 | 313 | 1 | M2OM_MOUSE |
| 24 | 432 | 26.7 | 313 | 1 | M2OM_BOVIN |
| 25 | 426 | 26.3 | 313 | 1 | M2OM_RAT |
| 26 | 416.5 | 25.7 | 287 | 1 | DIC_MOUSE |
| 27 | 415.5 | 25.6 | 287 | 1 | DIC_HUMAN |
| 28 | 327.5 | 20.2 | 324 | 1 | OACT_YEAST |
| 29 | 293 | 18.1 | 322 | 1 | SFC1_YEAST |
| 30 | 273 | 16.9 | 301 | 1 | MCAT_MOUSE |
| 31 | 272.5 | 16.8 | 311 | 1 | TXTP_RAT |
| 32 | 267 | 16.5 | 298 | 1 | ADT3_BOVIN |
| 33 | | | | | |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 265 | 16.4 | 298 | 1 | ADT3_HUMAN | P12236 homo sapien |
| 35 | 258 | 15.9 | 297 | 1 | ADT1_BOVIN | P02722 bos taurus |
| 36 | 258 | 15.9 | 301 | 1 | MCAT_RAT | P97521 rattus norv |
| 37 | 257 | 15.9 | 298 | 1 | ADT1_MOUSE | P49862 mus musculu |
| 38 | 257 | 15.9 | 301 | 1 | MCAT_HUMAN | O43772 homo sapien |
| 39 | 256.5 | 15.8 | 373 | 1 | Y1A6_YEAST | P40556 saccharomyc |
| 40 | 256 | 15.8 | 298 | 1 | ADT2_HUMAN | P05141 homo sapien |
| 41 | 256 | 15.8 | 300 | 1 | MCAT_ARATH | O93xm7 arabidopsi |
| 42 | 253 | 15.6 | 298 | 1 | ADT2_MOUSE | P51881 mus musculu |
| 43 | 252.5 | 15.6 | 311 | 1 | TXTP_BOVIN | P79110 bos taurus |
| 44 | 252.5 | 15.6 | 311 | 1 | TXTP_HUMAN | P53007 homo sapien |
| 45 | 252.5 | 15.6 | 339 | 1 | ADT_CHICK | P31692 Chlorella k |

ALIGNMENTS

| | | | | |
|----------|---|-----------|------|---------|
| RESULT 1 | UCP3_HUMAN | STANDARD; | PRT; | 312 AA. |
| ID | UCP3_HUMAN | | | |
| AC | P55916; O60475; O96HU3; | | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Mitochondrial uncoupling protein 3 (UCP 3). | | | |
| GN | UCP3 OR SLC5A9. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_Taxid=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Skeletal muscle; | | | |
| RX | MEDLINE=97324095; PubMed=9180264; | | | |
| RA | Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J., | | | |
| RA | Rossier C., Muzin P., Giacobino J.-P.; | | | |
| RT | "Uncoupling protein-3: a new member of the mitochondrial carrier | | | |
| RT | family with tissue-specific expression."; | | | |
| RL | FEBS Lett. 408:39-42(1997). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS UCP3L AND UCP3S). | | | |
| RX | MEDLINE=97450925; PubMed=9305858; | | | |
| RA | Gong D.-W., He Y., Karas W., Reisman M.; | | | |
| RT | "Uncoupling protein-3 is a mediator of thermogenesis regulated by | | | |
| RT | thyroid hormone, beta3-adrenergic agonists, and leptin."; | | | |
| RL | J. Biol. Chem. 272:24129-24132(1997). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=98158426; PubMed=9498661; | | | |
| RA | Uthamer S.A., Dalgaard L.T., Soerensen T.I.A., Tybjaerg-Hansen A., | | | |
| RA | Rehwal S.M., Andersen T., Clausen J.O., Pedersen O.; | | | |
| RT | "Organisation of the coding exons and mutational screening of the | | | |
| RT | uncoupling protein 3 gene in subjects with juvenile-onset obesity."; | | | |
| RL | Diabetologia 41:241-244(1998). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | PubMed=10958796; | | | |
| RA | Bieberhaer H., Oberkofler H., Krempner F., Strosberg A.D., Patsch W.; | | | |
| RT | "The uncoupling protein-3 gene is transcribed from tissue-specific | | | |
| RT | promoters in humans but not in rodents."; | | | |
| RL | J. Biol. Chem. 275:36394-36399(2000). | | | |
| RN | [6] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 3). | | | |
| RC | TISSUE=Skeletal muscle; | | | |
| RX | MEDLINE=22388257; PubMed=12477932; | | | |

DB 241 VKTRYNSPPGQYFSPFLDCMIMKVAOEGPTAFYKGFPSFLRLGSGNNVMMFTYBQLKRA 300
 QY 301 LMKVQMLRESPP 312
 DB 301 LMKVQMLRESPP 312

RESULT 2
 UCP3 CANFA STANDARD; PRT; 311 AA.
 ID UCP3 CANFA 09N219; 09TTS9;
 AC 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN SEQUENCE FROM N.A.
 RA Ishiooka K.;
 RT "Cloning of canine UCP families."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 14-146 FROM N.A.
 RA Thompson G.M., Kelly L.J., Candelore M.R.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; AB022020; BAA90458.1; -.
 DR EMBL; AF201378; AAF08310.1; -.
 DR InterPro; IPR002030; Mtc_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mtc_car; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 11 32
 FT TRANSMEM 77 99
 FT TRANSMEM 120 136
 FT TRANSMEM 183 199
 FT TRANSMEM 217 236
 FT TRANSMEM 271 293
 FT REPEAT 11 105
 FT REPEAT 114 205
 FT REPEAT 214 299
 FT DOMAIN 278 300
 FT CONFLICT 14 14 A > G (IN REF. 2).
 SQ SEQUENCE 311 AA; 34137 MW; A719PB8D66537502 CRC64;
 Query Match 92.1%; Score 1492.5; DB 1; Length 311;
 Best Local Similarity 91.7%; Pred. No. 2,9e-129;
 Matches 286; Conservative 14; Mismatches 11; Indels 1; Gaps 1;

QY 1 MWGLKSPDVPPTMAVYKFIAGTACPADLVTEPLDTAKYRLQIOGENQAVQTAFLVQYRG 60
 DB 1 MWGLKSPDVPPTTAVKFIAGTACPADLVTEPLDTAKYRLQIOGENQTAQARRQYRG 60
 QY 61 VLGTLITWRTGSPSPYNGVLVAGLQROMSPASIRIGLYDSKVQYTPGADNSSLITTR 120
 DB 61 VLGTLITWRTGSPSPYNGVLVAGLQROMSPASIRIGLYDSKVQYTPGADNSSLITTR 120
 QY 121 LAGCTGMAVTCOAQPTDVYKTRFQASIHLPGRSDRKSCTMDAYRTTAREGVGLWK 180
 DB 121 LAGCTGMAVTCOAQPTDVYKTRFQASIHLPGRSDRKSCTMDAYRTTAREGVGLWK 179
 QY 181 GLTPNTRMAVNCQAEVLYYDILKEKLDLHYHLLTDFPHFVSAGFGCATVVASPVV 240
 DB 180 GLTPNTRMAVNCQAEVLYYDILKEKLDLHYHLLTDFPHLISAFGAGCATVVASPVV 239
 QY 241 VKTRYNSPPGQYFSPFLDCMIMKVAOEGPTAFYKGFPSFLRLGSGNNVMMFTYBQLKRA 300
 DB 240 VKTRYNSPPGQYFSPFLDCMIMKVAOEGPTAFYKGFPSFLRLGSGNNVMMFTYBQLKRA 299
 QY 301 LMKVQMLRESPP 312
 DB 300 LMKVQMLRESPP 311

RESULT 3
 UCP3 PIG STANDARD; PRT; 308 AA.
 ID UCP3 PIG 09T649; 09XSE6;
 AC 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN SEQUENCE FROM N.A.
 RA Werner P., Nowaczyk K., Neuenschwander S., Strazinger G.;
 RL "Characterization of the porcine uncoupling proteins 2 and 3 (UCP2 &
 RL 3) and their localization to chromosome 9p by somatic cell hybrids."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Large white X Pietrain; TISSUE=Skeletal muscle;
 RA Damon M., Vincent A., Herpin P.;
 RT "First evidence of uncoupling protein (UCP) gene expression in piglet
 RT skeletal muscle."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF095744; AAD08811.1; -.

DR EMBL; AF128837; AAD33396.1; -;
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3_
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS50920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 74 96 2 (POTENTIAL).
 FT TRANSMEM 117 133 3 (POTENTIAL).
 FT TRANSMEM 180 196 4 (POTENTIAL).
 FT TRANSMEM 214 233 5 (POTENTIAL).
 FT TRANSMEM 268 290 6 (POTENTIAL).
 FT REPEAT 11 102 SOLCAR 1.
 FT REPEAT 111 202 SOLCAR 2.
 FT REPEAT 211 296 SOLCAR 3.
 FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).
 FT CONFLICT 7 8 PE -> SD (IN REF. 2).
 FT CONFLICT 13 13 T -> M (IN REF. 2).
 FT CONFLICT 17 17 L -> R (IN REF. 2).
 FT CONFLICT 49 49 A -> AVQT (IN REF. 2).
 FT CONFLICT 150 150 R -> G (IN REF. 2).
 SQ SEQUENCE 308 AA; 33772 MW; FDFLP28C28FDE397 CRC64;

Query Match 89.9%; Score 1457; DB 1; Length 308;
 Best Local Similarity 90.1%; Pred. No. 5, 1e-126;
 Matches 281; Conservative 14; Mismatches 13; Indels 4; Gaps 2;
 QY 1 MWGLKPSDVPPTMAVYKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60
 DB 1 MWGLKPSDVPPTMAVYKFLGAGTACFADLVTPPLDTAKVRLQIOGENQ---ARSAQYRG 57
 QY 61 VLGTLTMTWRTGSPSPNGVAGLORQMSFASIRIGLYDSKYQVYTPPGANSSLTTRI 120
 DB 58 VLGTLTMTWRTGSPSPNGVAGLORQMSFASIRIGLYDSKYQVYTPPGANSSLTTRI 117
 QY 121 LAGCTTGMAVYCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAYRTIAREGVGLMK 180
 DB 118 LAGCTTGMAVYCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAYRTIAREGVGLMK 176
 QY 181 GTLPNIMRNAIVNCAEVYTYDILKEKLDYHLLTDFNPFHVSAGAGCATVVASPDV 240
 DB 177 GTLPNITRNAIVNCAEMVYTYDILKEKLDYHLLTDFNPFHVSAGAGCATVVASPDV 236
 QY 241 VTRTYNNSPPGOYFSPDLDMIMVNAOEGPTAFYKGTSPFLALGSMNVYMTTYEQAKRA 300
 DB 237 VTRTYNNSPPGOYFSPDLDMIMVNAOEGPTAFYKGTSPFLALGSMNVYMTTYEQAKRA 296
 QY 301 LMKVQMLRESPP 312
 DB 297 LMKVQMLRESPP 308

RESULT 4
 UC33_BOVIN
 ID UC33_BOVIN STANDARD; PRT; 311 AA.
 AC 077792; Q9TVA1;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 3 (UCP 3).
 GN UCP3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;

RA Stone R.T., Smith T.P.L.;
 RT "Bovine uncoupling protein 3."
 RT Submitted (SSP-1998) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE OF 1-274 FROM N.A., AND VARIANT THR-53.
 RN Stone R.T., Rexroad C.E., Smith T.P.L.;
 RT "Bovine UCP2 and UCP3 map to BTA15."
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 solcar repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF092048; AAC61762.1; -;
 DR EMBL; AF127030; AAD33339.1; -;
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS50920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Polymorphism.
 FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 77 99 2 (POTENTIAL).
 FT TRANSMEM 120 136 3 (POTENTIAL).
 FT TRANSMEM 183 199 4 (POTENTIAL).
 FT TRANSMEM 217 236 5 (POTENTIAL).
 FT TRANSMEM 271 293 6 (POTENTIAL).
 FT REPEAT 11 105 SOLCAR 1.
 FT REPEAT 114 205 SOLCAR 2.
 FT REPEAT 214 299 SOLCAR 3.
 FT DOMAIN 278 300 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).
 FT VARIANT 53 53 A -> T.
 SQ SEQUENCE 311 AA; 34205 MW; BIAID26E25650D04 CRC64;

Query Match 87.6%; Score 1419.5; DB 1; Length 311;
 Best Local Similarity 87.2%; Pred. No. 1, 4e-122;
 Matches 272; Conservative 17; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MWGLKPSDVPPTMAVYKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60
 DB 1 MWGLKPSDVPPTMAVYKFLGAGTACFADLVTPPLDTAKVRLQIOGENQAVQTARLVQYRG 60
 QY 61 VLGTLTMTWRTGSPSPNGVAGLORQMSFASIRIGLYDSKYQVYTPPGANSSLTTRI 120
 DB 61 VLGTLTMTWRTGSPSPNGVAGLORQMSFASIRIGLYDSKYQVYTPPGANSSLTTRI 120
 QY 121 LAGCTTGMAVYCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAYRTIAREGVGLMK 180
 DB 121 LAGCTTGMAVYCAOPTDVVKVRFQASIHGSPSRDRTKSGTMDAYRTIAREGVGLMK 179
 QY 181 GTLPNIMRNAIVNCAEVYTYDILKEKLDYHLLTDFNPFHVSAGAGCATVVASPDV 240
 DB 180 GTLPNITRNAIVNCAEMVYTYDILKEKLDYHLLTDFNPFHVSAGAGCATVVASPDV 239
 QY 241 VTRTYNNSPPGOYFSPDLDMIMVNAOEGPTAFYKGTSPFLALGSMNVYMTTYEQAKRA 300

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DB 240 VSTRYVNSPPGQYHSPDCMLNMTQEGPTATYKGFTHSFLKLSGNNVMMFVYIEQMKRA 299
OY 301 LMKVQMLRESPP 312
DB 300 LMKVQMLRDSPP 311

RESULT 5
UCP3 RAT STANDARD; PRT; 308 AA.
AC P56499;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX MEDLINE=98074937; PubMed=9414126;
RA Matsuda J., Hosoda K., Itoh H., Son C., Doi K., Tanaka T.,
RA Fukunaga Y., Inoue G., Mishimura H., Yoshimasa Y., Yamori Y.,
RA Nakao K.;
RT "Cloning of rat uncoupling protein-3 and uncoupling protein-2 cDNAs:
RT their gene expression in rats fed high-fat diet.";
RT FEBS Lett. 418:200-204 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skeletal muscle;
RX MEDLINE=98165302; PubMed=9506477;
RA Boss O., Samet S., Desplanches D., Mayet M.-H., Seydoux J., Muzzin P.,
RA Giacobino J.-P.;
RT "Effect of endurance training on mRNA expression of uncoupling
RT proteins 1, 2, and 3 in the rat.";
RT PASEB J. 12:335-339 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RX MEDLINE=98400868; PubMed=9725803;
RA Lin B.-Z., Coughlin S., Pilch P.F.;
RT "Bidirectional regulation of uncoupling protein-3 and GLUT-4 mRNA in
RT skeletal muscle by cold.";
RT Am. J. Physiol. 275:E386-E391 (1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Skeletal muscle;
RA Solanes G., Valet P., Lowell B.B.;
RT "Lipopolysaccharide treatment increases thermogenesis and induces
RT uncoupling protein-3 gene expression in skeletal muscle.";
RT Submitted (OCT-1997) to the EMBL/GenBank/DBD databases.
RN [5]
RP FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
RP PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
RP DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
RP OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
RP ENERGY BALANCE (BY SIMILARITY).
RN [6]
RP SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
RP inner membrane (By similarity).
RN [7]
RP SIMILARITY: Belongs to the mitochondrial carrier family.
RN [8]
RP SIMILARITY: Contains 3 Solcar repeats.
RN [9]
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CC EMBL: AB006614; BAA23355.1; -
DR EMBL: U92069; AAB71523.1; -
DR EMBL: AF035943; AAC05740.1; -
DR EMBL: AF030163; AAD01891.1; -
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mito_carrier.
DR Pfam: PF00153; mlt_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PSS0920; SOLCAR_3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 74 96 2 (POTENTIAL).
FT TRANSMEM 117 133 3 (POTENTIAL).
FT TRANSMEM 180 196 4 (POTENTIAL).
FT TRANSMEM 214 233 5 (POTENTIAL).
FT TRANSMEM 268 290 6 (POTENTIAL).
FT REPEAT 11 102 SOLCAR 1.
FT REPEAT 111 102 SOLCAR 2.
FT REPEAT 211 296 SOLCAR 3.
FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).
SQ SEQUENCE 308 AA; 34014 MW; F86E784530AC555 CRC64;
Query Match 85.6%; Score 1386; DB 1; Length 308;
Best Local Similarity 86.2%; Pred. No. 1.6e-119;
Matches 269; Conservative 17; Mismatches 22; Indels 4; Gaps 2;
OY 1 MTGLRSDVPPPTMYAKYFAGTAGACADIVTEPLDTAKRLIOGEGNOAVQTRLVQYRG 60
DB 1 MWGLQSEVPPTTVKAFAGTAGACADIVTEPLDTAKRLIOGEGNOAVQTRLVQYRG 57
OY 61 VIGTLLTWRTGSPSPYNGVLVAGLQRMSPASIRIGLYDSYQVYTPKGADNSLTTRI 120
DB 58 VIGTLLTWRTGSPSPYNGVLVAGLQRMSPASIRIGLYDSYQVYTPKGADNSLTTRI 117
OY 121 LAGCTTGAAVTCAGPTDVYKTRFQASITLGSRSRKRSGMDAARTTAREGVGLWK 180
DB 118 LAGCTTGAAVTCAGPTDVYKTRFQASITLGSRSRKRSGMDAARTTAREGVGLWK 176
OY 181 GTLPNTRNAIYNCAEVVYDILKEKLDYHLTNDNPGHFSAFAGFCATVVASPDV 240
DB 177 GTLPNTRNAIYNCAEVVYDILKEKLDYHLTNDNPGHFSAFAGFCATVVASPDV 236
OY 241 VSTRYVNSPPGQYHSPDCMLNMTQEGPTATYKGFTHSFLKLSGNNVMMFVYIEQMKRA 300
DB 237 VSTRYVNSPPGQYHSPDCMLNMTQEGPTATYKGFTHSFLKLSGNNVMMFVYIEQMKRA 296
OY 301 LMKVQMLRESPP 312
DB 297 LMKVQMLRDSPP 308

RESULT 6
UCP3 MOUSE STANDARD; PRT; 308 AA.
AC P56501; O88293;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 3 (UCP 3).
GN UCP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sanchez D., Fleury C., Bouilland P., Riquier D.;
RT Submitted (NOV-1997) to the EMBL/GenBank/DBD databases.

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RN [2] SEQUENCE FROM N.A.
 RP STRAIN=Swiss Webster; TISSUE=Embryo;
 RX MEDLINE=98332721; PubMed=9666083;
 RA Yoshitomi H., Yamazaki K., Tanaka I.;
 RT "Cloning of mouse uncoupling protein 3 cDNA and 5'-flanking region,
 RL Gene 215:77-84(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Skeletal muscle;
 RA Grubic D., Zhan C.-Y., Sleiker L.J., Lowell B.B.;
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;
 RA Son C., Hosoda K., Matsuoka J., Nakao K.;
 RT "Cloning of mouse UCP3 cDNA."
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99167332; PubMed=10066417;
 RA Gong D.W., He Y., Reitman M.L.;
 RT "Genomic organization and regulation by dietary fat of the uncoupling
 RL protein 3 and 2 genes."
 RN [6]
 RP SEQUENCE OF 84-180 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Skeletal muscle;
 RX MEDLINE=96262957; PubMed=9600108;
 RA Shimokawa T., Kato M., Ezaki O., Hashimoto S.;
 RT "Transcriptional regulation of muscle-specific genes during myoblast
 RL differentiation."
 RN Biochem. Biophys. Res. Commun. 256:27-32(1999).
 RN [7]
 RP SEQUENCE OF 162-252 FROM N.A.
 RA Yan X., Ramsey T.G.;
 RT Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: UCP ARE MITOCHONDRIAL TRANSPORTER PROTEINS THAT CREATE
 CC PROTON LEAKS ACROSS THE INNER MITOCHONDRIAL MEMBRANE, THUS
 CC UNCOUPLING OXIDATIVE PHOSPHORYLATION. AS A RESULT, ENERGY IS
 CC DISSIPATED IN THE FORM OF HEAT. MAY PLAY A ROLE IN THE MODULATION
 CC OF TISSUE RESPIRATORY CONTROL. PARTICIPATES IN THERMOGENESIS AND
 CC ENERGY BALANCE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AF032902; AAB87084.1; -
 CC EMBL: AB010742; BAA25697.1; -
 CC EMBL: AF030164; AAD01892.1; -
 CC EMBL: AB008216; BAA33502.1; -
 CC EMBL: AF053352; AAC28328.1; -
 CC EMBL: AB011132; BAA31989.1; -
 CC EMBL: AF019883; AAB71543.1; -
 CC MGD: MG1:1099787; Ucp3.
 CC GO: GO:0005739; C:mitochondrion; IMP.
 CC GO: GO:0015302; F:uncoupling protein activity; IMP.
 CC GO: GO:0006631; P:fatty acid metabolism; IMP.
 CC GO: GO:000303; P:response to superoxide; IMP.
 CC InterPro: IPR002067; Mlt carrier.
 CC InterPro: IPR002030; Mlt uncoupling.
 CC InterPro: IPR001993; Mitoch carrier.
 CC Pfam: PF00153; mltc_cartr; 3.

DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 74 96 2 (POTENTIAL).
 FT TRANSMEM 117 133 3 (POTENTIAL).
 FT TRANSMEM 180 196 4 (POTENTIAL).
 FT TRANSMEM 214 233 5 (POTENTIAL).
 FT TRANSMEM 268 290 6 (POTENTIAL).
 FT REPEAT 11 102 SOLCAR 1.
 FT REPEAT 111 202 SOLCAR 2.
 FT REPEAT 211 296 SOLCAR 3.
 FT DOMAIN 275 297 PURINE NUCLEOTIDE BINDING (BY
 FT SIMILARITY).
 FT CONFLICT 179 179 W -> L (IN REF. 6).
 SQ SEQUENCE 308 AA; 33910 MM; 12CAD7674DFD0C3 CRC64;
 Query Match 84.8%; Score 1373; DB 1; Length 308;
 Best Local Similarity 85.6%; Pred. No. 2,56-118;
 Matches 267; Conservative 18; Mismatches 23; Indels 4; Gaps 2;
 QY 1 MVGLKPSDVPPTMAVKFAGTAGACPADLVTFPPIDTAKVRLQIGENQAVGTARLVQYRG 60
 DB 1 MVGLQPSSEVPTTVKFLGACTACPADLTFPIIDTAKVRLQIGENPGAGS---VQYRG 57
 QY 61 VLGTILTWRTGSPSPNGVLVAGLORQSPASIRIGLYDSVKQVYTPKGDNSLTTRI 120
 DB 58 VLGTILTWRTGSPSPNGVLVAGLORQSPASIRIGLYDSVKQVYTPKGDHSSVAIRI 117
 QY 121 LAGCTGAMAVTCAQPTDVVVRQASIHGSPSSDKYSGSTMAVRYTAAEEVGRGLMK 180
 DB 118 LAGCTTGMAVTCQPTDVVVRQAMIRLG-TGGERKRYGTMAVRYTAAEEVGRGLMK 176
 QY 181 GLTNIRKNAIVNCAEVYTDYILKEKLLDYHLTDNPFCHVSAFAGFCATVVASPDV 240
 DB 177 GTWPRITRNALVNCAMVTDYIIEKKLLBSLTFDNPCHVSAFAGFCATVVASPDV 236
 QY 241 VKTRYMNSPQGYSPDQCMKMAVQEGPTAFYKFTPSFLRLGSNVMVFYTYEQLKRA 300
 DB 237 VKTRYMNAFLGRYNSPLHCLMKMAVQEGPTAFYKGFVPSFLRLGAMNVMVFYTYEQLKRA 296
 QY 301 LMKQMLRESFP 312
 DB 297 LMKQVLALESFP 308
 RESULT 7
 UCP2_MOUSE STANDARD; PRT; 309 AA.
 AC P70406; O88285;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Mitochondrial uncoupling protein 2 (UCP 2) (UCHN).
 GN UCP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Muscle;
 RA Raimbault S., Bouillaud F., Ricquier D.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=97278985; PubMed=9133562;
 RA Gimeno R.E., Dembski M., Weng X., Deng N., Shyjan A.W.,
 RA Gimeno C.J., Iris F., Ellis S.J., Woolf E.A., Taragila L.A.;
 RT "Cloning and characterization of an uncoupling protein homolog: a
 RT potential molecular mediator of human thermogenesis."

Diabetes 46:900-906(1997).
 [3]
 RA SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA;
 RX MEDLINE=96374026; PubMed=9710252;
 RA Yamada M., Hashida T., Shibusawa N., Iwasaki T., Murakami M.,
 RA Menden T., Satoh T., Mori M.;
 RA "Genomic organization and promoter function of the mouse uncoupling
 RT protein 2 (UCP2) gene";
 RL FEBS Lett. 432:65-69(1998).
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Colon, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straube R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Mazny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
 proton leaks across the inner mitochondrial membrane, thus
 uncoupling oxidative phosphorylation from ATP synthesis. As a
 result, energy is dissipated in the form of heat (By similarity).
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- TISSUE SPECIFICITY: HIGHEST IN WHITE ADIPOSE TISSUE BUT ALSO
 DETECTED IN BROWN ADIPOSE TISSUE, HEART, AND KIDNEY. 4-6 TIMES
 HIGHER LEVELS ARE DETECTED IN OB/OB AND DB/DB MICE.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
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 CC -----
 CC EMBL: U69135; AAB17666.1; -
 DR EMBL: U94593; AAB53082.1; -
 DR EMBL: AB012159; BA32532.1; -
 DR EMBL: BC012697; AAH12697.1; -
 DR EMBL: BC012967; AAH12967.1; -
 DR MGD: MGI:109354; UCP2.
 DR InterPro: IPR002030; Mit uncoupling.
 DR InterPro: IPR001993; Mitoch carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS50920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 78 100 2 (POTENTIAL).
 FT TRANSMEM 120 136 3 (POTENTIAL).
 FT TRANSMEM 181 197 4 (POTENTIAL).
 FT TRANSMEM 215 234 5 (POTENTIAL).
 FT TRANSMEM 269 291 6 (POTENTIAL).

FT REPEAT 11 106 SOLCAR 1.
 FT REPEAT 114 203 SOLCAR 2.
 FT REPEAT 212 297 SOLCAR 3.
 FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY
 FT CONFLICT 285 285 V -> I (IN REF. 3).
 FT SEQUENCE 309 AA; 33373 MW; 329794EBA9810E5 CRC64;
 Query Match 71.9%; Score 1165.5; DB 1; Length 309;
 Best Local Similarity 72.8%; Pred. No. 2.6e-99;
 Matches 228; Conservative 31; Mismatches 49; Indels 5; Gaps 3;
 QY 1 NVGLKPSVPPPTMAVKFAGAGTACFADLVTEPLDTAKRLIQGENQA-VQTAIRLVQYR 59
 DB 1 NVGFRATDVPFAATKFKFAGATACIADITFPLDTAKRLIQGESQGLVTTAASQYR 60
 QY 60 GVLGTLITMVRREGCCSPNGVAGLQROMSASIRIGLYSDVKQYVTPKGDNSLTTR 119
 DB 61 GVLGTLITMVRREGSRSLNGVAGLQROMSPASVIRIGLYSDVKQFYT-KGSEHAGIGSR 119
 QY 120 ILAGCTGMAVTCAGPTDVVVFVFQASITLQPSRSDRKSQGTMDAVRTIAREEGVGLM 179
 DB 120 ILAGSTTGALAVAVAQPTDVVVFVFQQAQARAG--GGRYQSTVEAKYTIAREEGRGLM 176
 QY 180 KGTLEPNIEMNAIVNCAEVYVDILKELDYHLITDNPFCHEVSAFAGFCATVVASPD 239
 DB 177 KGTSPNVAARNAIIVNCAELVYVDILKOTLLKANLMTDDLPCHFTSAFAGFCCTVIASPD 236
 QY 240 VKTKYVNSPPQGYSPIDCMIKMAQSGPTAFYGGFTSPFLRLGSMVNVMTVEQLKR 299
 DB 237 VKTKYVNSALQGYSHAGCALTMLRKGPAPFAFYGFMSFLRLGSMVNVMTVEYQLKR 296
 QY 300 ALMKVQMLRESPE 312
 DB 297 ALMAAYQSHREAP 309
 RESULT 8
 UCP2_PIG STANDARD; PRT; 309 AA.
 AC 097562; Q96K29;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 2 (UCP 2).
 GN UCP2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=white adipose tissue;
 RA Werner P., Nowaczyk K., Neuenschwander S., Strazinger G.;
 RT "Characterization of the porcine uncoupling proteins 2 and 3 (UCP2 &
 RT 3) and their localization to chromosome 9p by somatic cell hybrids";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBD databases.
 RN [2]
 RP SEQUENCE OF 114-211 FROM N.A.
 RA Fang M.-Y., Zhao X.-B., Li N.;
 RT "Exon 3, Intron 3 and exon 4 sequencing of porcine uncoupling protein
 RT 2 gene";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
 proton leaks across the inner mitochondrial membrane, thus
 uncoupling oxidative phosphorylation from ATP synthesis. As a
 result, energy is dissipated in the form of heat (By similarity).
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----

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DR EMBL; AF036757; AAC05201.1; -
DR EMBL; AF332003; AAG45440.1; -
DR InterPro; IPR002030; Mit-uncoupling.
DR pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MTUNCouPLING.
DR PROSITE; PS50920; SOLCAR; 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 78 100 2 (POTENTIAL).
FT TRANSMEM 120 136 3 (POTENTIAL).
FT TRANSMEM 181 197 4 (POTENTIAL).
FT TRANSMEM 215 234 5 (POTENTIAL).
FT TRANSMEM 269 291 6 (POTENTIAL).
FT REPEAT 11 106 SOLCAR 1.
FT REPEAT 114 203 SOLCAR 2.
FT REPEAT 212 297 SOLCAR 3.
FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY
FT CONFLICT 115 115 G -> S (IN REF. 2).
FT CONFLICT 208 208 D -> N (IN REF. 2).
SQ SEQUENCE 309 AA; 33259 MW; 7A67D59946DA21BD CRC64;

Query Match
Best Local Similarity 71.6%; Score 1160.5; DB 1; Length 309;
Matches 227; Conservative 30; Mismatches 51; Indels 5; Gaps 3;

QY 1 MWGLKPSDVPPTMAVVFELAGTAACADLVTEPLDTAKVRLIOGEMQA-VQTAFLVQR 59
DB 1 MWGPKATEVPTATVVFELAGTAACADLVTEPLDTAKVRLIOGEMQA-VQTAFLVQR 60
QY 60 GVLGTLTWVRTEGSPSPNGVAVGQROMSPASITIGLYDSVKQVYTKKADNSLTTR 119
DB 61 GVLGTLTWVRTEGSPSPNGVAVGQROMSPASITIGLYDSVKQVYTKKADNSLTTR 119
QY 120 ILAGCTTGAAVATCAQPTDVVKVRFQASVHLGPRSDRKSGTMDAYRTIAEEGVRLM 179
DB 120 LINGSTTGAAVAVAOPTDVVKVRFQASVHLGPRSDRKSGTMDAYRTIAEEGVRLM 176
QY 180 KGTLPINMENAVNCAEVVYTDILKEKLDYHLITDNPCHPVSAFGAGCATVVASPYD 239
DB 177 KGTSPVAVANNAIVNCAELVYTDILKEKLDYHLITDNPCHPVSAFGAGCATVVASPYD 236
QY 240 VVKTRTNSPPQGYFPLDGMIMVAVOEPYAKFTTSFLTSGMNVMMPTVYRQLR 299
DB 237 VVKTRTNSAPPGYSAGHCALTMLOKEGPRAFYKFTPSFLTSGMNVMMPTVYRQLR 296
QY 300 ALMKVQLRESPPF 312
DB 297 ALMAAPASREAPF 309

RESULT 9
UCP2_RAT STANDARD; PRT; 309 AA.
AC P565F0; 070178; 088183;
DT 15-UTR-1998 (Rel. 36, Created)
DT 15-UTR-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 2 (UCP 2).
GN UCP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Strobel A., Stroberg A.D., Issad T.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brown adipose tissue;
RX MEDLINE=98074937; PubMed=9414126;
RA Matsuura J., Hosoda K., Itoh H., Son C., Doi K., Tanaka T.,
RA Fukunaga Y., Inoue G., Nishimura H., Yoshimasa Y., Yamori Y.,
RA Nakao K.;
RT "Cloning of rat uncoupling protein-3 and uncoupling protein-2 cDNAs:
RT their gene expression in rats fed high-fat diet.";
RL FEBS Lett. 418:200-204(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
RA Yamazaki K., Yoshimoto H., Tanaka T.;
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Mouse; TISSUE=Brain;
RX MEDLINE=98173791; PubMed=9512646;
RA Hidaka S., Kakuma T., Yoshimatsu H., Yasunaga S., Kurokawa M.,
RA Sakata T.;
RT "Molecular cloning of rat uncoupling protein 2 cDNA and its expression
RT in genetically obese Zucker fatty (fa/fa) rats.";
RL Biochim. Biophys. Acta 1389:178-186(1998).
CC -1- FUNCTION: UCP acts as mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of organs, with
CC predominant expression in the heart, lung and spleen.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC -----
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CC EMBL; AF036757; AAC98733.1; -
CC EMBL; AB006613; BAA23383.1; -
CC EMBL; AB010743; BAA25698.1; -
CC EMBL; AB005143; BAA28832.1; -
CC InterPro; IPR002030; Mit-uncoupling.
CC InterPro; IPR001993; Mitoch_carrier; 3.
CC pfam; PF00153; mito_carr; 3.
CC PRINTS; PR00784; MTUNCouPLING.
CC PROSITE; PS50920; SOLCAR; 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 78 100 2 (POTENTIAL).
FT TRANSMEM 120 136 3 (POTENTIAL).
FT TRANSMEM 181 197 4 (POTENTIAL).
FT TRANSMEM 215 234 5 (POTENTIAL).
FT TRANSMEM 269 291 6 (POTENTIAL).
FT REPEAT 11 106 SOLCAR 1.
FT REPEAT 114 203 SOLCAR 2.
FT REPEAT 212 297 SOLCAR 3.
FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY
FT CONFLICT 9 9 V -> L (IN REF. 4).
FT CONFLICT 268 268 A -> T (IN REF. 3).
SQ SEQUENCE 309 AA; 33376 MW; 3297935CF97A0E CRC64;

Query Match 71.4%; Score 1156.5; DB 1; Length 309;
 Best Local Similarity 72.2%; Pred. No. 1.7e-98;
 Matches 226; Conservative 32; Mismatches 50; Indels 5; Gaps 3;

QY 1 MVGLKSDVPTMAVFLAGTACACADLVTPPLDTRAKVRLQIQENQAV-QTAPLVQYR 59
 1 MVGPKATDVPATATVFLGAGTACIADITPLDTRAKVRLQIQSSQGLARFASQYR 60
 DB 1 MVGPKATDVPATATVFLGAGTACIADITPLDTRAKVRLQIQSSQGLARFASQYR 60
 QY 60 GVLGTLTVNRTEGCPSPNGVLVAGIQRQMSFASITIGLYDSKYQYTPKGDNSLITR 119
 61 GVLGTLTVNRTEGCPSPNGVLVAGIQRQMSFASITIGLYDSKYQYTPKGDNSLITR 119
 DB 61 GVLGTLTVNRTEGCPSPNGVLVAGIQRQMSFASITIGLYDSKYQYTPKGDNSLITR 119
 QY 120 ILAAGCTGMAATVCAPTDVKVRFQASITLGPSSDRKSGTMDVYRTAREEGVGLM 179
 120 ILAAGCTGMAATVCAPTDVKVRFQASITLGPSSDRKSGTMDVYRTAREEGVGLM 179
 DB 120 ILAAGCTGMAATVCAPTDVKVRFQASITLGPSSDRKSGTMDVYRTAREEGVGLM 179
 QY 180 KGTLPINENAVINCAVVTYDILKEKLDYHLLTDFPCFVSAFAGCATVVASPD 239
 177 KGTSPVAVANAIINCELVYDILKOTLTKANIMTDLPCHFSARQAGPCTVVASPD 236
 DB 177 KGTSPVAVANAIINCELVYDILKOTLTKANIMTDLPCHFSARQAGPCTVVASPD 236
 QY 240 VVKTRFMNSPGQYFEPDLDMIMQAOEGPTAFYKGTFTSEFLGSMNVMTTYEQLR 239
 237 VVKTRFMNSPGQYFEPDLDMIMQAOEGPTAFYKGTFTSEFLGSMNVMTTYEQLR 236
 DB 237 VVKTRFMNSPGQYFEPDLDMIMQAOEGPTAFYKGTFTSEFLGSMNVMTTYEQLR 236
 QY 300 ALMKVQMLRESP 312
 297 ALMAAYESREAP 309
 DB 297 ALMAAYESREAP 309

RESULT 10
 UC2P2_HUMAN STANDARD; PRT; 309 AA.
 ID UC2P2_HUMAN STANDARD; PRT; 309 AA.
 AC P55851;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial uncoupling protein 2 (UCP 2) (UCPF).
 GN UCP2 OR SLC25A8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE=97324095; PubMed=9180264;
 RA Boss O., Samec S., Paoloni-Giacobino A., Dulloo A., Seydoux J.,
 RA Rossier C., Muzzin P., Giacobino J.-P.;
 RT "uncoupling protein-3: a new member of the mitochondrial carrier
 RT family with tissue-specific expression.";
 RL FEBS Lett. 408:39-42(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skeletal muscle;
 RA MEDLINE=97207646; PubMed=9054939;
 RA Fleury C., Neverova M., Collins S., Raimbault S., Champigny O.,
 RA Levi-Meyrueis C., Bouillaud F., Seldin M.F., Surwit R.S.,
 RA Ricquier D., Warden C.H.;
 RT "uncoupling protein-2: a novel gene linked to obesity and
 RT hyperinflammation.";
 RL Nat. Genet. 15:269-272(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-55.
 RC TISSUE=Spleen;
 RA MEDLINE=97278985; PubMed=9133562;
 RA Gimeno R.E., Dembeki M., Weng X., Deng N., Shyjan A.W.,
 RA Cloning and characterization of an uncoupling protein homolog: a
 RT potential molecular mediator of human thermogenesis.";
 RL Diabetes 46:900-906(1997).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-55.

RA Klammemark M., Orho M., Groop L.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98227655; PubMed=9568704;
 RA Argyropoulos G., Brown A.M., Peterson R., Likes C.E., Watson D.K.,
 RA Garvey W.T.;
 RT "Structure and organization of the human uncoupling protein 2 gene and
 RT identification of a common biallelic variant in Caucasian and African-
 RT American subjects.";
 RL Diabetes 47:685-687(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99185293; PubMed=10082652;
 RA Requeux C., Cassard-Douclier A.M., Raimbault S., Miroux B.,
 RA Fleury C., Gelly C., Bouillaud F., Ricquier D.;
 RT "Functional organization of the human uncoupling protein-2 gene, and
 RT juxtaposition to the uncoupling protein-3 gene";
 RL Biochem. Biophys. Res. Commun. 255:40-46(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Butterfield Y.S.N., Grimwood J., Schmutz J., Myers R.M.,
 RA Schenker A., Schein J.E., Jones S.U.M., Maita M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
 CC proton leaks across the inner mitochondrial membrane, thus
 CC uncoupling oxidative phosphorylation from ATP synthesis. As a
 CC result, energy is dissipated in the form of heat.
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult human tissues,
 CC including tissues rich in macrophages. Most expressed in white
 CC adipose tissue and skeletal muscle.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solcar repeats.
 CC -----
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 CC -----
 DR EMBL; U62819; AAC5136.1; -;
 DR EMBL; U76367; AAB4841.1; -;
 DR EMBL; U94592; AAB5309.1; -;
 DR EMBL; AJ223477; CA11402.1; -;
 DR EMBL; AJ223478; CA11402.1; -;
 DR EMBL; AJ223479; CA11402.1; JOINED.
 DR EMBL; AF019409; AAC39690.1; -;
 DR EMBL; AF096289; AAD21151.1; -;

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DR EMBL: BC011737; AAH11737.1; -.
DR Genew: HGNC:12518; UCP2.
DR MIM: 601693;
DR GO: GO:0015302; F:uncoupling protein activity; TAS.
DR GO: GO:0015992; P:proton transport; TAS.
DR InterPro: IPR002030; Mlt uncoupling.
DR InterPro: IPR001993; Mlt carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR; 3.
DR KMW: Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Polymorphism.
FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 78 100 2 (POTENTIAL).
FT TRANSMEM 120 136 3 (POTENTIAL).
FT TRANSMEM 181 197 4 (POTENTIAL).
FT TRANSMEM 215 234 5 (POTENTIAL).
FT TRANSMEM 269 291 6 (POTENTIAL).
FT REPEAT 11 106 SOLCAR 1.
FT REPEAT 114 203 SOLCAR 2.
FT REPEAT 212 297 SOLCAR 3.
FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).
FT VARIANT 55 55 A -> V (in dbSNP:660339).
FT CONFLICT 219 219 T -> I (IN REF. 2).
SQ SEQUENCE 309 AA; 33229 MM; 2E1741391621E3D9 CRC64;

Query Match
Best Local Similarity 71.0%; Score 1149.5; DB 1; Length 309;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

1 MWGLKPSDVPPTMAVKFELGAGTACACADIVTPEPLDTAKVRLQIOGENQA-VQTARLVQYR 59
1 MWGLKPSDVPPTMAVKFELGAGTACACADIVTPEPLDTAKVRLQIOGENQA-VQTARLVQYR 60
60 GVLGTTILMTVRTEGPCSPYNGIYAGIQRQMSFASIRIGLYDSVKQYVTPKGDNSLTLR 119
61 GVMGTTILMTVRTEGPCSPYNGIYAGIQRQMSFASIRIGLYDSVKQYVTPKGDNSLTLR 119
120 ILAGCTTGAMAVTCAQPTDVVVRFOASIHILGPSRSDRYSGTMAVYRTIAREEGVGLM 179
120 ILAGCTTGAMAVTCAQPTDVVVRFOASIHILGPSRSDRYSGTMAVYRTIAREEGVGLM 176
180 KGTLPNIMNNAIYNCAEVVYTDILKEKLDYHLTNPCHPVSAGAFCAIVASPYD 239
177 KGTSPVARNNAIYNCAELVYTDILKDALIKANIMTDDLPCHFTSFAAGAFCTTVIASPYD 236
240 VKTRRYMNSPPQGYRSPIDCMIKMVAQSGPTAFYKGFTSFRLSGMNVMMFVTVYQLR 299
237 VKTRRYMNSALQYSSAGHCALTMLOKGPRAFYKGFMSFRLSGMNVMMFVTVYQLR 296
QY 300 ALMKVQMLRESPF 312
DB 297 ALMAACTSREAPF 309

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RT "Cloning of canine UCP families."
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 4-197 FROM N.A.
RA Thompson G.M., Kelly L.J., Candefiore M.R.
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB020887; BAA30457.1; -.
DR EMBL: AF201377; AAF08309.1; -.
DR InterPro: IPR002030; Mlt uncoupling.
DR InterPro: IPR001993; Mlt carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR; 3.
DR KMW: Mitochondrion; Transmembrane; Repeat.
FT TRANSMEM 11 32 1 (POTENTIAL).
FT TRANSMEM 78 100 2 (POTENTIAL).
FT TRANSMEM 120 136 3 (POTENTIAL).
FT TRANSMEM 181 197 4 (POTENTIAL).
FT TRANSMEM 215 234 5 (POTENTIAL).
FT TRANSMEM 269 291 6 (POTENTIAL).
FT REPEAT 11 106 SOLCAR 1.
FT REPEAT 114 203 SOLCAR 2.
FT REPEAT 212 297 SOLCAR 3.
FT DOMAIN 276 298 PURINE NUCLEOTIDE BINDING (BY SIMILARITY).
FT CONFLICT 64 64 C -> G (IN REF. 2).
SQ SEQUENCE 309 AA; 33270 MM; D9860F0EAB870BF CRC64;

Query Match
Best Local Similarity 70.7%; Score 1145.5; DB 1; Length 309;
Matches 227; Conservative 29; Mismatches 52; Indels 5; Gaps 3;

1 MWGLKPSDVPPTMAVKFELGAGTACACADIVTPEPLDTAKVRLQIOGENQA-VQTARLVQYR 59
1 MWGLKPSDVPPTMAVKFELGAGTACACADIVTPEPLDTAKVRLQIOGENQA-VQTARLVQYR 60
60 GVLGTTILMTVRTEGPCSPYNGIYAGIQRQMSFASIRIGLYDSVKQYVTPKGDNSLTLR 119
61 GVMGTTILMTVRTEGPCSPYNGIYAGIQRQMSFASIRIGLYDSVKQYVTPKGDNSLTLR 119
120 ILAGCTTGAMAVTCAQPTDVVVRFOASIHILGPSRSDRYSGTMAVYRTIAREEGVGLM 179
120 ILAGCTTGAMAVTCAQPTDVVVRFOASIHILGPSRSDRYSGTMAVYRTIAREEGVGLM 176
180 KGTLPNIMNNAIYNCAEVVYTDILKEKLDYHLTNPCHPVSAGAFCAIVASPYD 239
177 KGTSPVARNNAIYNCAELVYTDILKDALIKANIMTDDLPCHFTSFAAGAFCTTVIASPYD 236
240 VKTRRYMNSPPQGYRSPIDCMIKMVAQSGPTAFYKGFTSFRLSGMNVMMFVTVYQLR 299
237 VKTRRYMNSALQYSSAGHCALTMLOKGPRAFYKGFMSFRLSGMNVMMFVTVYQLR 296
QY 300 ALMKVQMLRESPF 312
DB 297 ALMAACTSREAPF 309

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RESULT 12
UCP2_CYPCA STANDARD; PRT; 310 AA.
ID _ucp2_cypca
AC 09w725;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 2 (UCP 2).
GN UCP2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Stuart J.A., Harper J.A., Brindle K.M., Brand M.D.;
RT "Uncoupling protein 1 homologues and thermogenesis? UCP2 from cold-
RT blooded vertebrates."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: AJ243486; CAB46248.1; -.
DR InterPro: IPR002030; Mitc_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mitco_cartr/ 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR/ 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 79 101
FT TRANSMEM 121 137
FT TRANSMEM 182 198
FT TRANSMEM 216 235
FT TRANSMEM 270 292
FT REPEAT 11 107
FT REPEAT 115 204
FT REPEAT 213 298
FT REPEAT 277 299
FT DOMAIN
SQ SEQUENCE 310 AA; 33532 MW; AD0B4D73C73704E CRC64;
Query Match 69.2%; Score 1121; DB 1; Length 310;
Best Local Similarity 72.4%; Pred. No. 3.1e-95;
Matches 220; Conservative 31; Mismatches 47; Indels 6; Gaps 4;
QY 1 MYGLKSDVPTMAVFLGAGTACFADVTFPLDPAKYLQIGENO-AVQFAR-LVOY 58
DB 1 MNGFRAGDVPPRTATVFAGTACADLFTPLDPAKYLQIGSSKIPVNGHPVK 60
QY 59 RGVLGITLITVARTGFCSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPKGDNSLTT 118
DB 61 RGVFGITSTVREVGSRSLYSGLVAGLQROMSPASVRIGLYDSVKQFYT-KGSEHVGIGS 119
QY 119 RILAGCTTGAMAVTCAQPTDVVAVRFOASIHGSPSRSDRYSGTMDAYRTIAEBCVRL 178

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RESULT 13
UCP2_BRARE STANDARD; PRT; 310 AA.
ID _ucp2_brare
AC 09w720;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitochondrial uncoupling protein 2 (UCP 2).
GN UCP2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Stuart J.A., Harper J.A., Brindle K.M., Brand M.D.;
RT "Uncoupling protein 1 homologues and thermogenesis? UCPS from cold-
RT blooded vertebrates."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
CC proton leaks across the inner mitochondrial membrane, thus
CC uncoupling oxidative phosphorylation from ATP synthesis. As a
CC result, energy is dissipated in the form of heat (By similarity).
CC -1- SUBUNIT: Acts as a dimer forming a proton channel (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC -----
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CC -----
EMBL: AJ243250; CAB46268.1; -.
DR ZFIN: ZDB-GENE-990708-8; ucp2.
DR InterPro: IPR002030; Mitc_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mitco_cartr/ 3.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS50920; SOLCAR/ 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 11 32
FT TRANSMEM 79 101
FT TRANSMEM 121 137
FT TRANSMEM 182 198
FT TRANSMEM 216 235
FT TRANSMEM 270 292
FT REPEAT 11 107
FT REPEAT 115 204
FT REPEAT 213 298
FT REPEAT 277 299
FT DOMAIN
QY 120 RLMGCTTGAMAVFLAQTVDVVKVRFOAONSAG---ANKRHYGTDAVRTIAKEGFRGL 176
QY 179 WKGTLPNTRNAIYNCAEVVTTIDIKKELDYLITDNFPCHFAVAFGAGFATVVASPV 238
DB 177 WKGTSPNITRNAIYNCTELVYDILKDALILKSLMTDLPCHFTSAFGAGFCTVYIASPV 236
QY 239 DVVKTRVNSPPGQYFSPLDCKIKVNAQEGPTAFYKGFPTSPFLRGSNNVVFVYVYBOLK 298
DB 237 DVVKTRVNSAPGQYCSALNCANMLTKBPAFYKGFPTSPFLRGSNNVVFVYVYBOLK 296
QY 299 RALM 302
DB 297 RALM 300

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SQ SEQUENCE 310 AA; 33573 MW; 1A2F82FA2CB1DD1 CRC64;

Query Match 69.0%; Score 1117; DB 1; Length 310;
 Best Local Similarity 69.3%; Pred. No. 7.2e-95;
 Matches 217; Conservative 35; Mismatches 55; Indels 6; Gaps 3;

QY 1 MVGLKPSDVPPTMVKFLGAGTACFADLVTFPPDIAKVRLOIGENQAVQTARLVYRG 58
 DB 1 MVGFRAQGVPPPTATKFIAGAGTACIADLFPPDIAKVRLOIGENQASTMGKPKY 60

QY 59 RGVLTGTTMTRTGPGCPYNGVLVAGLORQMSFASIRIGLYDSVKQYTPKGDNSLTTR 118
 DB 61 RGVLTGTTMTRTGPGCPYNGVLVAGLORQMSFASIRIGLYDSVKQYTPKGDNSLTTR 119

QY 119 RILGCTTGAMAVTCAOPTDVVYRFOASIHGFSRDRKSGTMDARTTAREGVNGL 178
 DB 120 RILGCTTGAMAVTCAOPTDVVYRFOASIHGFSRDRKSGTMDARTTAREGVNGL 176

QY 179 WKGTLFNIMRNAIVNCAEVVTVYDILKEKLDYHLTDNPFCHVSAFGAFCAVVASPV 238
 DB 177 WKGTLFNIMRNAIVNCAEVVTVYDILKEKLDYHLTDNPFCHVSAFGAFCAVVASPV 236

QY 239 DVVKTIRYNSAPGQYFSPDCKMKVNAQEGPTAFYKGFPSFLRIGSNVNVFVYEQLK 298
 DB 237 DVVKTIRYNSAPGQYFSPDCKMKVNAQEGPTAFYKGFPSFLRIGSNVNVFVYEQLK 296

QY 299 RALMKVQMLRSP 311
 DB 297 RALMKVQMLRSP 309

RESULT 14

UCP1_RABBIT STANDARD; PRT; 306 AA.
 ID UCP1_RABBIT
 AC P14271;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Mitochondrial brown fat uncoupling protein 1 (UCP 1) (Thermogenin).
 GN UCP1 OR UCP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89273628; PubMed=2730654;
 RA Balogh A.G., Ridley R.G., Patel H.V., Freeman K.B.;
 RT "Rabbit brown adipose tissue uncoupling protein mRNA: use of only one
 of two polyadenylation signals in its processing.";
 RL Biochem. Biophys. Res. Commun. 161:156-161(1989).
 CC -1- FUNCTION: UCP are mitochondrial transporter proteins that create
 proton leaks across the inner mitochondrial membrane, thus
 uncoupling oxidative phosphorylation from ATP synthesis. As a
 result, energy is dissipated in the form of heat.
 CC -1- SUBUNIT: Acts as a dimer forming a proton channel.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- TISSUE SPECIFICITY: Brown adipose tissue.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -1- SIMILARITY: Contains 3 Solar repeats.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL; X14696; CAA32826.1; -;
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.

DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS50920; SOLCAR; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 11 32 1 (POTENTIAL).
 FT TRANSMEM 74 96 2 (POTENTIAL).
 FT TRANSMEM 116 132 3 (POTENTIAL).
 FT TRANSMEM 178 194 4 (POTENTIAL).
 FT TRANSMEM 212 231 5 (POTENTIAL).
 FT TRANSMEM 266 288 6 (POTENTIAL).
 FT REPEAT 11 102 SOLCAR 1.
 FT REPEAT 110 200 SOLCAR 2.
 FT REPEAT 209 294 SOLCAR 3.
 FT DOMAIN 273 295 PURINE NUCLEOTIDE BINDING
 (BY SIMILARITY).
 SQ SEQUENCE 306 AA; 33083 MW; 58343CAD94C910F1 CRC64;

Query Match 56.7%; Score 919; DB 1; Length 306;
 Best Local Similarity 58.7%; Pred. No. 9.8e-77;
 Matches 178; Conservative 47; Mismatches 72; Indels 6; Gaps 3;

QY 1 MVGLKPSDVPPTMVKFLGAGTACFADLVTFPPDIAKVRLOIGENQAVQTARLVYRG 60
 DB 1 MVGTTTDDVPPTMGVKTFISAGVAACLDVTFPPDIAKVRLOIGEPPTSG---IRYKG 57

QY 61 VLGTTILMTWRTGCPSPYNGVLVAGLORQMSFASIRIGLYDSVKQYTPKGDNSLTTRI 120
 DB 58 VLGTTILMTWRTGCPSPYNGVLVAGLORQMSFASIRIGLYDSVKQYTPKGDNSLTTRI 116

QY 121 LAGCTTGAMAVTCAOPTDVVYRFOASIHGFSRDRKSGTMDARTTAREGVNGL 180
 DB 117 LAGCTTGAMAVTCAOPTDVVYRFOASIHGFSRDRKSGTMDARTTAREGVNGL 174

QY 181 GTLFNMNAIVNCAEVVTVYDILKEKLDYHLTDNPFCHVSAFGAFCAVVASPV 240
 DB 175 GTLFNMNAIVNCAEVVTVYDILKEKLDYHLTDNPFCHVSAFGAFCAVVASPV 234

QY 241 VKTRYNNSPQGYFSPDCKMKVNAQEGPTAFYKGFPSFLRIGSNVNVFVYEQLK 300
 DB 235 VKTRYNNSPQGYFSPDCKMKVNAQEGPTAFYKGFPSFLRIGSNVNVFVYEQLK 294

QY 301 LMK 303
 DB 295 LMR 297

RESULT 15

UCP1_HUMAN STANDARD; PRT; 307 AA.
 ID UCP1_HUMAN
 AC P25874; Q13218;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mitochondrial brown fat uncoupling protein 1 (UCP 1) (Thermogenin).
 GN UCP1 OR UCP OR SLC25A7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9038166; PubMed=2380264;
 RA Casard A.M., Bouilland F., Matted M.-G., Hentz E., Raimbault S.,
 RT "Human uncoupling protein gene: structure, comparison with rat gene,
 RT and assignment to the long arm of chromosome 4.";
 RL J. Cell. Biochem. 43:255-264(1990).
 RN [2]
 RP REVISIONS.
 RA Bouilland F.;
 RL Submitted (Jul-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

